

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	2030	100.0	2030	6	AX548023	Sequence	
2	2030	100.0	2042	6	AX548024	Sequence	
3	2030	100.0	111945	8	ATFC12	Arabidops	
4	2030	100.0	198427	8	ATCHR152	Arabidops	
5	1064	52.4	1064	6	AX509457	Sequence	
6	211.8	10.4	288	11	AL807890	Arabidops	
7	211.8	10.4	290	11	BX295033	Arabidops	
8	95.4	4.7	1001	8	AY086004	Arabidops	
9	93	4.6	348174	3	CR382399	Plasmodi	
10	91.2	4.5	135203	9	AC035278	Homo sapi	
11	90.2	4.4	8056	6	AX599046	Sequence	
12	89.4	4.4	104992	2	AC005504	Plasmodi	
13	89.4	4.4	169546	2	AC004157	Plasmodi	
14	89.4	4.4	250421	3	AE014849	Plasmodi	
15	89.2	4.4	26565	2	AC119399	Homo sapi	
16	88.4	4.4	115218	9	HL159A1	Human DNA	
17	88.4	4.4	136240	3	AC117070	Dityostoc	
18	87	4.3	195319	2	CR388410	Danio rerio	
19	86.8	4.3	1496	3	CEY5312D	Caenorhal	

Query Match 100.0%; Score 2030; DB 6; Length 2042; Best Local Similarity 100.0%; Pred. No. 1.6e-292; Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CTTCATAGAGGATGGACCAATGAAGAATACCTCTCTTTCTATTTTATTTGATTTAG	60						
Db	7	CTTCATAGAGGATGGACCAATGAAGAATACCTCTCTTTCTATTTTATTTGATTTAG	66						
Qy	61	AAAAATCATATTCATTTACAAAAGGAAAAAAAATAATTTTGTATCCTTAAAGTTATAC	120						
Db	67	AAAAATCATATTCATTTACAAAAGGAAAAAAAATAATTTTGTATCCTTAAAGTTATAC	126						
Qy	121	TTACAAATTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTGG	180						
Db	127	TTACAAATTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTGG	186						
Qy	181	TTTTAGGAAAAATGTATCTTTTCATATAAAAATATATAGATCTTCAAAGAACTGAAT	240						
Db	187	TTTTAGGAAAAATGTATCTTTTCATATAAAAATATATAGATCTTCAAAGAACTGAAT	246						
Qy	241	GGGTTTTCAACTATTTTATCGTTTGCACACTACTTTGACTTATCAAAAAGAGTTCAAATA	300						
Db	247	GGGTTTTCAACTATTTTATCGTTTGCACACTACTTTGACTTATCAAAAAGAGTTCAAATA	306						
Qy	301	GA AAAATAGAAATCGAATCACAGTTTCAGTCTGTAAGGGGATTCATATTCGTCGACATTT	360						
Db	307	GA AAAATAGAAATCGAATCACAGTTTCAGTCTGTAAGGGGATTCATATTCGTCGACATTT	366						
Qy	361	TAAAGAGTTGTTTGTGTTTTTTTTTCCAAATCTGCAATGTTTTTTCGTTCCGTTGAACCAAT	420						
Db	367	TAAAGAGTTGTTTGTGTTTTTTTTTCCAAATCTGCAATGTTTTTTCGTTCCGTTGAACCAAT	426						
Qy	421	TCAACACTTTGTATAAACCGAATAGTAATATATCTAGACGTACGCAATATACAAAATAAA	480						
Db	427	TCAACACTTTGTATAAACCGAATAGTAATATATCTAGACGTACGCAATATACAAAATAAA	486						
Qy	481	ATTAAACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATACGCAACCTA	540						
Db	487	ATTAAACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATACGCAACCTA	546						
Qy	541	GAATATCAATGAAATTTTAAATCGAGGATAATCAATATCCAACTCAACGATATACAAAAGC	600						
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Qy	601	CTAATAATAGATCAATGAAATCAAAATAACTAAACATAGTAATATACATTTGTTGTTA	660						
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Qy	661	AACAGAAATATATACATTAATAATAGTATGAAATAATGAATATATATAGATTAAGAGGGTA	720						
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Qy	721	TATGTTTACAACCTACAGATCACCATCCACAAATTTAAACAATCCGATTTGGCGGGCCATGTT	780						
Db	727	TATGTTTACAACCTACAGATCACCATCCACAAATTTAAACAATCCGATTTGGCGGGCCATGTT	786						
Qy	781	TCGATATTTGCCAACCTGATTTGATGTGACTGCCAGCTGGCATATTTTCCCTCCTGAT	840						
Db	787	TCGATATTTGCCAACCTGATTTGATGTGACTGCCAGCTGGCATATTTTCCCTCCTGAT	846						
Qy	841	ACGTTTTTACCCCTTCTCTCTGTTTCAACCGTTAATTTCAATTTTATTTGACCGCT	900						
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Qy	901	GTCTTTTACCGTTTTTAAAGAAAACCGAACCGAATCATTAACATACCGAATCACATGT	960						
Db	907	GTCTTTTACCGTTTTTAAAGAAAACCGAACCGAATCATTAACATACCGAATCACATGT	966						
Qy	961	CTTCATGGTGACGTAAACAGACTTATTTTCCGGTTTGAATTTGGTTTAACTTATGAGATT	1020						
Db	967	CTTCATGGTGACGTAAACAGACTTATTTTCCGGTTTGAATTTGGTTTAACTTATGAGATT	1026						

Qy	1021	GTGCTAACCCGAAAAACAGAAACGGTATTATGACGCCAAACGAGCGAAGAGGGGTAAACACGAA	1081
Db	1027	GTGCTAACCCGAAAAACAGAAACGGTATTATGACGCCAAACGAGCGAAGAGGGGTAAACACGAA	1086
Qy	1081	AGAGGGGATGCGACAAATCGTAATTAACAAGGAAAAATAAAGGGGTGGTTTTCCACGATAAGTC	1140
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Qy	1141	TGTCTATATATGACGCGAAAGGGTTCCTTTAAATTCAGAGAGACAATTAATACAGTTTCGTTG	1200
Db	1147	TGTCTATATATGACGCGAAAGGGTTCCTTTAAATTCAGAGAGACAATTAATACAGTTTCGTTG	1206
Qy	1201	TTTGGAGAAGAAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATTCGTT	1260
Db	1207	TTTGGAGAAGAAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATTCGTT	1266
Qy	1261	TCAAGTAGTCTCTTTTATCAAACTCTTAATATAAACAAATCAAAACATGAACACGCTCGTG	1320
Db	1267	TCAAGTAGTCTCTTTTATCAAACTCTTAATATAAACAAATCAAAACATGAACACGCTCGTG	1326
Qy	1321	TCCTTCGTTTCGATTCAGATACGATTTTTTTAGTTTCATGTGAATGAACCTCTGTTTTATTAC	1380
Db	1327	TCCTTCGTTTCGATTCAGATACGATTTTTTTAGTTTCATGTGAATGAACCTCTGTTTTATTAC	1386
Qy	1381	TACTAGGGTGTTCAAATATTTTTCCGAGAAATACCAGAGGAAACAAAGTTAGTGATATAT	1440
Db	1387	TACTAGGGTGTTCAAATATTTTTCCGAGAAATACCAGAGGAAACAAAGTTAGTGATATAT	1446
Qy	1441	TGATCGACAGTATAGAGTAATTTATACATAAATCATGTTTGTCTCAAGCATCTACGTT	1500
Db	1447	TGATCGACAGTATAGAGTAATTTATACATAAATCATGTTTGTCTCAAGCATCTACGTT	1506
Qy	1501	TGAAATATATATAAGAAAGTTTTTTTTTGGTGGAATAAATATGTATGAGAAAGTTTCATCTTTC	1560
Db	1507	TGAAATATATATAAGAAAGTTTTTTTTTGGTGGAATAAATATGTATGAGAAAGTTTCATCTTTC	1566
Qy	1561	ATAATAGTGAAACAACTCTCTTTTCATACCAAAAAAATAATTTGAAAAAAATTTAGTGAAA	1620
Db	1567	ATAATAGTGAAACAACTCTCTTTTCATACCAAAAAAATAATTTGAAAAAAATTTAGTGAAA	1626
Qy	1621	CTCTCTTTGTCGATTAGTTAGGTTTGGACTCAGAATCAAAATACGATTTAGCATACAA	1680
Db	1627	CTCTCTTTGTCGATTAGTTAGGTTTGGACTCAGAATCAAAATACGATTTAGCATACAA	1686
Qy	1681	ATTTTTTGGCATGGCAATTTATGTCGAGGTAAATATATCAATAGAAACATATTTTTTA	1740
Db	1687	ATTTTTTGGCATGGCAATTTATGTCGAGGTAAATATATCAATAGAAACATATTTTTTA	1746
Qy	1741	GGAGTAGTTAAGATTATGATTTGAAGAAATACATTTAGCATAGCATATAAAATTTTCTTTG	1800
Db	1747	GGAGTAGTTAAGATTATGATTTGAAGAAATACATTTAGCATAGCATATAAAATTTTCTTTG	1806
Qy	1801	CTGTTCTTGGTTTTGTCGTTTTATAGAACATTTGAAATATGTAATTTTTTTTTTTCACCC	1860
Db	1807	CTGTTCTTGGTTTTGTCGTTTTATAGAACATTTGAAATATGTAATTTTTTTTTTTCACCC	1866
Qy	1861	AGTAGATATGTAATACACATAGTAAGTAACATGGTAGTTTATATAGAGAGAGATTGTA	1920
Db	1867	AGTAGATATGTAATACACATAGTAAGTAACATGGTAGTTTATATAGAGAGAGATTGTA	1926
Qy	1921	TTTTTTCGTATATTTCTTTTGTGAAAAATAAATATGTGTAAAAATTTATTTGTTTATTAATTT	1980
Db	1927	TTTTTTCGTATATTTCTTTTGTGAAAAATAAATATGTGTAAAAATTTATTTGTTTATTAATTT	1986
Qy	1981	GACAGATTTGTTTCAGCTTGAGAGGTTTAAATTTAGATTAAACCAACAAAAAG 2030	
Db	1987	GACAGATTTGTTTCAGCTTGAGAGGTTTAAATTTAGATTAAACCAACAAAAAG 2036	
RESULT 3			
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LOCUS Arabidopsis thaliana DNA chromosome 4 BAC clone F1C12.1ESSA			
DESCRIPTION ATFLIC12			

137674	pb		GAATAATCAATGAAATTTAAATCGAGGATAAATCAATATCCAATCTCAACGATAATCAAAAGC	137733
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661	Qy		AACAGAAATAATACATTTAATAGTATGAAATAATGAATATAAATGAGATAAGAGCGGTA	720
137794	Db		AACAGAAATAATACATTTAATAGTATGAAATAATGAATATAAATGAGATAAGAGCGGTA	137853
721	Qy		TATGTTACAACTACAGATCACATCCACAAATTAAACCAATCCGATTCGGTGGCGCCATTTGT	780
137854	Db		TATGTTACAACTACAGATCACATCCACAAATTAAACCAATCCGATTCGGTGGCGCCATTTGT	137913
781	Qy		TCGATATTTGCCAACTGATTTGATGTGACCTGCCAGCTGGCATATTTTCCCCTCTCGATT	840
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841	Qy		ACGTTTTTACCCTTTCCCTCTCTGTTTTCACCGTTAAATTCAAATTTTACTATTTGTACCCGT	900
137974	Db		ACGTTTTTACCCTTTCCCTCTCTGTTTTCACCGTTAAATTCAAATTTTGTACCCGT	138033
901	Qy		GTCCTTTCACCTTTTAAAGAAAAACCAACCCGAAATCATACTATACCGAAATCATAGT	960
138034	Db		GTCCTTTCACCTTTTAAAGAAAAACCAACCCGAAATCATACTATACCGAAATCATAGT	138093
961	Qy		CTTTCATGGTGACGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAACTTATCAGATT	1020
138094	Db		CTTTCATGGTGACGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAACTTATCAGATT	138153
1021	Qy		GTGCTAACCCGAAAAACAGAAAAACGGTTATGACGCCAACAGGCAAGAGGGTAAAAACGAGAA	1080
138154	Db		GTGCTAACCCGAAAAACAGAAAAACGGTTATGACGCCAACAGGCAAGAGGGTAAAAACGAGAA	138213
1081	Qy		AGGGGATGTCAGAAATCGTAATTAAACAAGAAAAATAAAGGGTGGTTTCACGATAAGTC	1140
138214	Db		AGGGGATGTCAGAAATCGTAATTAAACAAGAAAAATAAAGGGTGGTTTCACGATAAGTC	138273
1141	Qy		TGCTATATGACCGGAAAGGGTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTGTG	1200
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1201	Qy		TTTCGAGAAGAAGAACACAGATCAAAATCAGAGGAGAGATCTCTAAAGAGATTTATCGTT	1260
138334	Db		TTTCGAGAAGAAGAACACAGATCAAAATCAGAGGAGAGATCTCTAAAGAGATTTATCGTT	138393
1261	Qy		TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACACGTCGTG	1320
138394	Db		TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACACGTCGTG	138453
1321	Qy		TCCTCGTTTCGATTCATAGATAGATTTTTTATAGTCAATGTAATGAACTCTGTTTATTAC	1380
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1381	Qy		TACTAGGGTCTGTTCAATATTTTTCCGAGAAATTTACCAGAGGAACAAAGTTAGTGATTATAT	1440
138514	Db		TACTAGGGTCTGTTCAATATTTTTCCGAGAAATTTACCAGAGGAACAAAGTTAGTGATTATAT	138573
1441	Qy		TGATGCAGAGTATGAAGTAATTTATATACATAAATCATGTTTGTGTTCTCAAGCATCTAGT	1500
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1501	Qy		TGAAATATATATAAGAGTGTTTTTTTTGGTGAAAAAATATGTATGAGAGTTTCATCTTTC	1560
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1561	Qy		ATATAGTGAACAACCTCTCTTTTCATACCAAAAAAATTTGAAAAAATAATAGTGAA	1620
138694	Db		ATATAGTGAACAACCTCTCTTTTCATACCAAAAAAATTTGAAAAAATAATAGTGAA	138753
1621	Qy		CTCTCTTTGTCGGAATTAGGTTTAGGTTTGGACTCAGAATCAAAATACGATTAGCATAAACAA	1680

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Qy	1741	GGAGTAGTTAAGAT	TATGATTGAAGAAATACATACTATTACGATTAAGCATATAAAATTTTCTTTTG	1800
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Qy	1861	AGTAGATATGTACT	TATACACATAAAGTAACATGGGTAGTTTATATAGAGAGAGATTGGA	1920
Db	138994	AGTAGATATGTACT	TATACACATAAAGTAACATGGGTAGTTTATATAGAGAGAGATTGGA	139053
Qy	1921	TTTTTTCGTAAT	TTTCTTTTGGTTGTTGAAAATATAAATATGTGTAAAAATTTTATTGTTTATTAAATTT	1980
Db	139054	TTTTTTCGTAAT	TTTCTTTTGGTTGTTGAAAATATAAATATGTGTAAAAATTTTATTGTTTATTAAATTT	139113
Qy	1981	GACAGATTTGTT	TCAGTTTGGAAGTTTAAATTTAGATTTAAACAAACAAAAAG	2030
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RESULT 5				
AX509457				
LOCUS	AX509457	1064 bp	DNA	linear PAT 27-SEP-2002
DEFINITION	Sequence 4152 from Patent WO0216655.			
ACCESSION	AX509457			
VERSION	AX509457.1	GI:23390694		
KEYWORDS				
SOURCE				
ORGANISM				
Arabidopsis thaliana (Chale cress)				
Arabidopsis thaliana				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi				
1				
Harper, J.P.; Kreps, J., Wang, X. and Zhu, T.				
Stress-regulated genes of plants, transgenic plants containing same, and methods of use				
Patent: WO 0216655-A 4152 28-FEB-2002;				
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)				
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ORIGIN				
Query Match	52.4%	Score 1064;	DB 6;	Length 1064;
Best Local Similarity	100.0%	Pred. No. 7.3e-149;		
Matches 1064;	Conservative	0;	Mismatches	0; Indels
0;	Gaps	0;		
Qy	967	GGTGACGTAA	CACAGACTTATTTCCGGTTGAAATTTGGTTTAAACCTATTAGATTGTGCTA	1026
Db	1	GGTGACGTAA	CACAGACTTATTTCCGGTTGAAATTTGGTTTAAACCTATTAGATTGTGCTA	60
Qy	1027	ACCGAAACAGAA	ACGGTTATGACGCCAACGACGAGGGGTAACAGAGAGAGAGGG	1086
Db	61	ACCGAAACAGAA	ACGGTTATGACGCCAACGAGGCAAGGGGTTAAACAGAGAGAGAGGG	120
Qy	1087	GATGGCAGAAAT	CGTAATTAAACAAAGGAAATTAAGGGTGGTTTTCACGATAAGTCTGTCTA	1146
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Qy	1147	TATGACCGGAA	AGGGTTCTTTAAATTCAGAGAGACAATTAATCAGTTTCGTGTGTTTGA	1206
Db	181	TATGACCGGAA	AGGGTTCTTTAAATTCAGAGAGACAATTAATCAGTTTCGTGTGTTTGA	240

dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3'-end of the transposon, _5 denotes a sequence derived from the 5'-end of the transposon. BBSRC GARNET, ATIS project
On-line seed stock requests: <http://nasc.nott.ac.uk/NASC/stockcode/N120195>.

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FEATURES
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ORIGIN
    Query Match      10.4%; Score 211.8; DB 11; Length 290;
    Best Local Similarity 99.1%; Pred. No. 4.8e-22;
    Matches 213; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1161 GTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTTTCGAGAGAGAGAGAAC 1220
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Db 215 GTTCCATAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTTTCGAGAGAGAGAGAAC 156

Qy 1221 GATCAAAATACGAGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAAGTCTCTTTATCA 1280
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Db 155 GATCAAAATACGAGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAAGTCTCTTTATCA 96

Qy 1281 AACTCTTAATTAACAAATCAAAACATGACACGTGCTGCTCTGTTTCGATCTTAGAT 1340
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Db 95 AACTCTTAATTAACAAATCAAAACATGACACGTGCTGCTCTGTTTCGATCTTAGAT 36

Qy 1341 ACGATTTTGTAGTTCATGTGAATGAATCTGTTTT 1375
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Db 35 ACGATTTTGTAGTTCATGTGAATGAATCTGTTTT 1

RESULT 8
AY086004          1001 bp mRNA linear PLN 14-APR-2003
LOCUS
Arabidopsis thaliana clone 20592 mRNA, complete sequence.
ACCESSION
AY086004
VERSION
AY086004.1 GI:21404714
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1001)
Haas,B.J., Volkovsky,N., Town,C.D., Troupkan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE
22088475
PUBMED
12093376
REFERENCE
2 (bases 1 to 1001)
Brover,V., Troupkan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1001)
Brover,V., Troupkan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of

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the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. GenSet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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FEATURES
    Location/Qualifiers
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ORIGIN
    Query Match      4.7%; Score 95.4; DB 8; Length 1001;
    Best Local Similarity 81.0%; Pred. No. 7.2e-05;
    Matches 111; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db 1 AGAGAGACAAATTAATCAGTTTCGTGTGTTTGGAGAGAGAGAGAGAGAGATCAATACGAG 60

Qy 1234 GAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAAGTCTCTTTATCAAACTTTAATATA 1293
    |||
Db 61 GAGAGATCTCTAAAGAGATTTATCGTTTCAAAATTTGTTACGTTGAGAGAGTTAATTAG 120

Qy 1294 AACAAATCAAAACATCA 1310
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Db 121 ATTAACAACAACAAAAGA 137

RESULT 9
CR382399/c
LOCUS
Plasmodium falciparum chromosome 6, complete sequence; segment 2/5.
ACCESSION
CR382399.1
VERSION
CR382399.1 GI:46361038
KEYWORDS
HTG.
SOURCE
Plasmodium falciparum 3D7
ORGANISM
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 348174)
Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D.,
Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K.,
Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C.,
Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C.,
Cronin,A., Davies,R., Davis,P., Dear,P., Dearden,F., Doggett,J.,
Feltwell,T., Goble,A., Goodhead,I., Gwilliam,R., Hamlin,N.,
Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S.,
Horrocks,P., Humphray,S., Jagels,K., James,K.D., Johnson,D.,
Kerhornou,A., Knights,A., Konfortov,B., Kyes,S., Larke,N.,
Lawson,D., Lennard,N., Line,A., Maddison,M., McLean,J., Mooney,P.,
Moule,S., Murphy,L., Oliver,K., Ormond,D., Price,C., Quail,M.A.,
Rabinovitsch,E., Rajandream,M.A., Rutter,S., Rutherford,K.M.,
Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R.,
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Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
 Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
 Nature 419 (6906), 527-531 (2002)
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 2 (bases 1 to 348174)
 Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K., Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and Barrell, B.G.
 Unpublished
 3 (bases 1 to 348174)
 Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K., Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and Barrell, B.G.
 Direct Submission
 Submitted (20-SEP-2002) P. falciparum Genome Sequencing Consortium, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
 4 (bases 1 to 348174)
 Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K., Berry, A.E., Berriman, M., RA Pain, A., Hall, N., Atkin, R., Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and Barrell, B.G.
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 Submitted (26-MAR-2004) P. falciparum Genome Sequencing Consortium, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
 For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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TITLE
Genome sequence of the human malaria parasite Plasmodium falciparum
JOURNAL
Nature 419 (6906), 498-511 (2002)
MEDLINE
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PUBMED
12368864
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AUTHORS
Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M., Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
TITLE
Direct Submision
JOURNAL
Submitted (13-SEP-2002) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
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ACCESSION AC119199
VERSION AC119199.1 GI:20330813
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 26565)
          DOE Joint Genome Institute.
          Submitted (26-APR-2002) Production Sequencing Facility, DOE Joint
          Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
          -----Genome Center
          Center: Joint Genome Institute
          Center Code: JGI
          Web site: http://www.jgi.doe.gov
          -----
          Project Information
          Center Project Name: 32002, FOS36972
          Center clone name: LLNL-FOS_21E4
          -----
          Summary Statistics
          Consensus quality: 23959 bases at least Q40
          Consensus quality: 25069 bases at least Q30
          Consensus quality: 25752 bases at least Q20
          Estimated insert size: 43700; agarose-fp estimation
          Estimated insert size: 26465; sum-of-contigs estimation
          Quality coverage: 8.47 in Q20 bases; agarose-fp estimation
          Quality coverage: 13.99 in Q20 bases; sum-of-contigs estimation.
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 2 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *
          * 1 2369: contig of 2369 bp in length
          * 2370 2465: gap of unknown length
          * 2470 26565: contig of 24096 bp in length.
          Location/Qualifiers
            1..26565
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              /chromosome="19"
              /clone="LLNL19FOS-21E4"

FEATURES
    source
        13 ATGGACCAATTTGAGAAATACCTTCTCTTTCTATTTTATTTTATTTGATTTAGAAAAATCATATTC 72
        5929 ATATATAATTATACATAACTGTATTAATAATATAATAATAATAATAATAATAATAATAATA 5870
        73 ATTACAAAAGGAAAAAAATAATTTTTTGTATCTCTAAAGTTATATACTTTACAAATTTTCC 132
        5869 AATATACATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATTA 5810
        133 ACATTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGGTTTAGGAAAAA 192
        5809 TTATATATATAGTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5750
        193 TGTATCTTTTTCATATAAAAAATATAGATCTTCAAGAAACTGAATTTGGTTTTCAACT 252
        5749 TATAATATATATAATATGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5690

Query Match 4.4%; Score 89.2; DB 2; Length 26565;
Best Local Similarity 45.8%; Pred. No. 0.00027;
Matches 342; Conservative 0; Mismatches 403; Indels 1; Gaps 1;

QY 13 ATGGACCAATTTGAGAAATACCTTCTCTTTCTATTTTATTTTATTTGATTTAGAAAAATCATATTC 72
Db 5929 ATATATAATTATACATAACTGTATTAATAATATAATAATAATAATAATAATAATAATAATAATA 5870
QY 73 ATTACAAAAGGAAAAAAATAATTTTTTGTATCTCTAAAGTTATATACTTTACAAATTTTCC 132
Db 5869 AATATACATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATTA 5810
QY 133 ACATTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGGTTTAGGAAAAA 192
Db 5809 TTATATATATAGTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5750
QY 193 TGTATCTTTTTCATATAAAAAATATAGATCTTCAAGAAACTGAATTTGGTTTTCAACT 252
Db 5749 TATAATATATATAATATGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5690
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QY 253 ATTTTATCGTTTGACACTACTTTTGACTTATCAAAAAGAGTTCAAAATAGAAAATAGAAT 312
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QY 313 CGAATCACACAGTTTTCAGTGTGAAGAGGGAATTTGATATTTGGTCGACATTTTAAAGAGTTGTT 372
Db 5629 ATAAATTATATTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5570
QY 373 TTGTTTTTTTTTCCAAATCTGCATGGTTTTTTCGTTCCGTTGAACCAAAATTCACACACTTTGT 432
Db 5569 ATATAATAATTTATATACCTATATATATTAATAATAATAATAATAATAATAATAATAATAATA 5510
QY 433 ATAAACGGATAGTAAATATATACAGCTAGCGCAATACCAAAAATAAAATTAACACTCAA 492
Db 5509 CATATAATTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 5450
QY 493 TTCACAAATTTGAATCTACACCATATCATGCATATATATCAGCAACCTAGAGTAATCAATG 552
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QY 553 AAATTTAATCGAGGATAATCAATATCCAACTCAACGATTAATCAAAAGCCCTAAATAATAGAT 612
Db 5389 TAATATGTATAATTTATATACCTATAT-AAATTTATTTATTAATTTTATATAATAATAATAATA 5331
QY 613 CAATGAATCAAAATAACTAAACATAGTAAATATACATTTGTTTGTAAACAGATAATA 672
Db 5330 CATATAAAATTTATTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5271
QY 673 TACATTATATAGTATGAAAAATATGAATATAATGAGATAAGAGCGGTATATGTTTACAAC 732
Db 5270 TATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5211
QY 733 ACAGATCCACCATCCCAATTAACAAT 758
Db 5210 ATAAATTTATTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5185
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Search completed: October 24, 2005, 00:50:34
Job time : 8766 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: October 23, 2005, 14:50:52 ; Search time 1093 Seconds
(without alignments)
10994.579 Million cell updates/sec

Title: US-10-643-676-1
Perfect score: 2030
Sequence: 1 cttcatgaagatggacca.....ttagattaaacaacaaaaag 2030

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
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8: geneseqn2003as:.*
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10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004as:.*
13: geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	2030	100.0	2042	6	ABZ75216 Arabidops
3	1064	52.4	1064	6	ABZ16347 Arabidops
4	95.4	4.7	999	3	AAC49043 Arabidops
5	95.4	4.7	1001	3	AAC37034 Arabidops
6	93.4	4.6	495	3	AAC38110 Arabidops
7	90.2	4.4	8056	8	ABZ10246 Haematopo
8	88.4	4.4	115218	8	ACA64845 Human HNR
9	87.4	4.3	515	3	AAC52118 Arabidops
10	82.8	4.1	8056	8	ABZ10100 Haematopo
11	79	3.9	8056	8	ABZ10246 Haematopo
12	78.8	3.9	15548	6	ABZ134155 Human imm
13	76	3.7	9810	6	ABZ132426 Human imm
14	75.4	3.7	8961	6	ABZ28428 DNA trans
15	75.4	3.7	8961	6	ABZ49380 Human pol
16	74.4	3.7	110000	13	ABD32968_6
17	74.2	3.7	5413	4	AAS46694 Tumour su
18	73.2	3.6	6242	6	ABZ134148 Human imm
19	72.4	3.6	19634	8	ABZ10015 Haematopo
20	72.4	3.6	19634	8	ABZ10161 Haematopo

C 21	72.4	3.6	19634	13	ADS89671	Ad889671 Oligonuc1
C 22	72.4	3.6	19634	13	ADS89397	Ad889397 Oligonuc1
C 23	72.2	3.5	478	13	ACN51993	Acn51993 Cotton an
C 24	72	3.5	10682	6	ABN80085	Abn80085 Human che
C 25	71.8	3.5	8056	8	ABZ10100	Abz10100 Haematopo
C 26	71.8	3.5	110000	6	ABA92787_3	Continuation (4 of
C 27	71.4	3.5	883	4	AAL15210	Aal15210 Human bre
C 28	71.4	3.5	960	11	ACN85231	Acn85231 Breast ca
C 29	71	3.5	529	13	ACN56029	Acn56029 Cotton an
C 30	71	3.5	1501	8	ABZ10188	Abz10188 Haematopo
C 31	71	3.5	1501	10	ADE84162	Ade84162 Human lym
C 32	70.8	3.5	5979	4	AAS45313	Aas45313 Chemical
C 33	70.8	3.5	5979	6	ABK28152	Abk28152 DNA trans
C 34	69.4	3.4	11964	6	ABQ67025	Abq67025 Human ang
C 35	69.4	3.4	158001	12	ADL17884	Adl17884 Human pho
C 36	69.2	3.4	110000	13	ABD32968_6	Continuation (7 of
C 37	69	3.4	12610	13	ADS89699	Ad889699 Oligonuc1
C 38	69	3.4	13286	13	ADS89730	Ad889730 Oligonuc1
C 39	68.8	3.4	7498	6	ABL33257	Ab133257 Human imm
C 40	68.8	3.4	19787	6	ABL33451	Ab133451 Human imm
C 41	68.8	3.4	20420	4	AAK73165	Aak73165 Human imm
C 42	68.8	3.4	20420	6	ABK69933	Abk69933 Human sec
C 43	68.6	3.4	5286	13	ADS89278	Ad889278 Oligonuc1
C 44	68.2	3.4	14023	6	ABL34105	Ab134105 Human imm
C 45	67.8	3.3	6071	6	ABL32325	Ab132325 Human imm

ALIGNMENTS

RESULT 1
ABZ75215
ID ABZ75215 standard; cDNA; 2030 BP.

AC ABZ75215;

DT 23-APR-2003 (first entry)

DE Arabidopsis thaliana endomembrane associated promoter cDNA.

KW ENDO; endomembrane associated; promoter; expression; gene; ss.

OS Arabidopsis thaliana.

PN WO200268665-A2.

PD 06-SEP-2002.

PF 14-FEB-2002; 2002WO-EP002894.

PR 22-FEB-2001; 2001US-0270779P.

XX (RHOB-) RHOBIO.

XX Thomas T, Nuccio M, Hsieh T;

DR WPI; 2002-707007/76.

PT New isolated ENDO promoter from the gene of Arabidopsis thaliana, useful for directing expression of genes in plants.

XX Claim 1; Page 17; 18pp; English.

PS The invention relates to the novel isolated Arabidopsis thaliana endomembrane associated (ENDO) gene promoter sequence. The nucleic acid is useful for directing expression of genes in plants. The present sequence represents the A. thaliana ENDO promoter of the invention

CC Sequence 2030 BP; 722 A; 287 C; 319 G; 702 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 2030; DB 6; Length 2030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAAATCATATTCATTACAAAAGGAAAAAATAAATTTTTTGTGATCCTAAAGTTATAAC 120
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QY 121 TTACAAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTTGG 180
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QY 181 TTTTAGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATT 240
DB 181 TTTTAGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATT 240
QY 241 GGGTTTTTCAACTATTTTATCGTTTGGACACTTCTTGTGACTTATCAAAAAGAGTTCAAAATA 300
DB 241 GGGTTTTTCAACTATTTTATCGTTTGGACACTTCTTGTGACTTATCAAAAAGAGTTCAAAATA 300
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DB 301 GAAAAATAGAAATCGAATCACACGTTTTCAGTGTAAAGAGGATTTGATATTTGGTCGACATTT 360
QY 361 TAAAGAGTTGTTGTTTTTTTTTCCAAATCTGCATGTTTTTCCGTTGGAACCAAAAT 420
DB 361 TAAAGAGTTGTTGTTTTTTTTTCCAAATCTGCATGTTTTTCCGTTGGAACCAAAAT 420
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DB 481 ATTAATACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATCAGCAACCTA 540
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DB 541 GAATAATCAATGAAATTTAATCGAGGATATCAATATCCAACTCAACGATTAATCAAAAGC 600
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DB 601 CTAATAATAGATCAATGAAATTTAATCGAGGATATCAATATCCAACTCAACGATTAATCAAAAGC 660
QY 661 AACAGAAATAATACATTATAATAGTATGAAAAATATGAATATATATGAGATAAGAGGCGTA 720
DB 661 AACAGAAATAATACATTATAATAGTATGAAAAATATGAATATATATGAGATAAGAGGCGTA 720
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QY 781 TCGATATTTCCCAACTGTGATTTGATGTGACTGCCAGCTGGCAVATTTTCCCTCCTCGATT 840
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QY 961 CTTTCATGGTCAGTGAACAGACTTTATTTTCCGGTTGAAATTTGGTTTAACTATTTGAGATT 1020
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DB 1021 GTGCTAACCGAAAAACAGAAAACGGTTATGACGCCAACGAGGCAAGAGGGGTAAAAACGAGAA 1080
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DB 1141 TGTCTATATGACCGCGAAAGGGTTTCTTAAATTCAGAGAGACAATTAATCAGTTTTCGTGTG 1200
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DB 1201 TTTGGAGAGAAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTT 1260
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DB 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAAATATAAAACAAATCAAAACATGAACACGTCGTG 1320
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QY 1501 TGAATATATATATAAGAAAGTTTTTTTTTGGTGAATAAATATGTATGAGAAAGTTTCATCTTTC 1560
DB 1501 TGAATATATATAAGAAAGTTTTTTTTTGGTGAATAAATATGTATGAGAAAGTTTCATCTTTC 1560
QY 1561 ATAAATAGTGAACCAACTCTCTTTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAA 1620
DB 1561 ATAAATAGTGAACCAACTCTCTTTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAA 1620
QY 1621 CTCTCTTGTCCGATTTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATAAACAA 1680
DB 1621 CTCTCTTGTCCGATTTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATAAACAA 1680
QY 1681 ATTTTTTGGCATGGCAATTTATTTGTCGAGGTAAAAATATATACCAATAGAAACATATTTTGA 1740
DB 1681 ATTTTTTGGCATGGCAATTTATTTGTCGAGGTAAAAATATATACCAATAGAAACATATTTTGA 1740
QY 1741 GGAGTAGTTAAGATTTATGATGAAGAAATATCTATTAGCATAGCAATAAAAATTTTCTTTTG 1800
DB 1741 GGAGTAGTTAAGATTTATGATGAAGAAATATCTATTAGCATAGCAATAAAAATTTTCTTTTG 1800
QY 1801 CTGCTCTTGGTTTTTCTCGTTTTTATAGAACATTTGATCTATTTGTTTTTTTTTTCACC 1860
DB 1801 CTGCTCTTGGTTTTTCTCGTTTTTATAGAACATTTGATCTATTTGTTTTTTTTTTCACC 1860
QY 1861 AGTAGATATGTACTATACACACATTAAGTAACATCGGTTAGTTTATATAGAGAGAGATTTGA 1920
DB 1861 AGTAGATATGTACTATACACACATTAAGTAACATCGGTTAGTTTATATAGAGAGAGATTTGA 1920
QY 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAAATGATGTGAAAAATTTATTTGTTTAAATTT 1980
DB 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAAATGATGTGAAAAATTTATTTGTTTAAATTT 1980
QY 1981 GACAGATTTGTTCCACGTTGAGAAAGTTTTAAATTTAGATTTAAACACAAAAAG 2030
DB 1981 GACAGATTTGTTCCACGTTGAGAAAGTTTTAAATTTAGATTTAAACACAAAAAG 2030
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RESULT 2
ABZ75216
ID ABZ75216 standard; cDNA; 2042 BP.
XX ABZ75216;
XX ABZ75216;
DT 23-APR-2003 (first entry)
XX
```


QY 1621 CTCTCTTTGTCGGATTAGGTTAGGTTGGACTCAGAACTCAAAATACGATTAGCATACAA 1680
DB |||||
QY 1627 CTCTCTTTGTCGGATTAGGTTAGGTTGGACTCAGAACTCAAAATACGATTAGCATACAA 1686
DB |||||
QY 1681 ATTTTTTGGCATGGCAATATTGTTCTCGAGGTAAATATATACCAATAGAAACATATTTTA 1740
DB |||||
QY 1687 ATTTTTTGGCATGGCAATATTGTTCTCGAGGTAAATATATACCAATAGAAACATATTTTA 1746
DB |||||
QY 1741 GGAGTAGTAAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAATTTCTTTTG 1800
DB |||||
QY 1747 GGAGTAGTAAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAATTTCTTTTG 1806
DB |||||
QY 1801 CTGTTCTTGGTTTTGTCGTTTATAGAACATTCGAATATGTAATTTGTTTTTTTTCACC 1860
DB |||||
QY 1807 CTGTTCTTGGTTTTGTCGTTTATAGAACATTCGAATATGTAATTTGTTTTTTTTCACC 1866
DB |||||
QY 1861 AGTAGATATGTACTATACACATAAGTAACTGGGTAGTTTATATAGAGAGAGATTGA 1920
DB |||||
QY 1921 TTTTTCGTATATTTCTTTGTTGAAATTAATATGTTGTAATAATTTATGTTTATTAATTT 1980
DB |||||
QY 1927 TTTTTCGTATATTTCTTTGTTGAAATTAATATGTTGTAATAATTTATGTTTATTAATTT 1986
DB |||||
QY 1981 GACAGATTGTTGTCAGTTGAGAGCTTTAAATTTAGATTAAACAAACAAAAG 2030
DB |||||
QY 1987 GACAGATTGTTGTCAGTTGAGAGCTTTAAATTTAGATTAAACAAACAAAAG 2036
DB |||||

RESULT 3
ABZ16347
ID ABZ16347 standard; DNA; 1064 BP.
XX
AC ABZ16347;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4152.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN W0200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 14; SEQ ID NO 4152; 577pp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1064 BP; 375 A; 126 C; 197 G; 366 T; 0 U; 0 Other;
Query Match 52.4%; Score 1064; DB 6; Length 1064;
Best Local Similarity 100.0%; Pred. No. 3.4e-170; Indels 0; Gaps 0;
Matches 1064; Conservative 0; Mismatches 0;
QY 967 GGTGACGTAAACAGACTTATTTTCGGTTGCAATTTGTTTAACTATTGTGAGATTGCTA 1026
DB |||||
QY 1027 ACCGAAAAACAGAAACGGTTATGACGCCAACGAGGCAAGGGGTAAACAGAGAAAGGG 1086
DB |||||
QY 1087 GATGGCAGAAATCGTAATTAACAAGGAAATAAAGGTGGTTTTCAGATAAGTCTGTCTA 1146
DB |||||
QY 121 GATGGCAGAAATCGTAATTAACAAGGAAATAAAGGTGGTTTTCAGATAAGTCTGTCTA 180
QY 1147 TATGACGCCGAAAGGGTTTCTTAAATTCAGAGACAAATTAATCAGTTTCGTGTGTTGGA 1206
DB |||||
QY 181 TATGACGCCGAAAGGGTTTCTTAAATTCAGAGACAAATTAATCAGTTTCGTGTGTTGGA 240
QY 1207 GAAGAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTTCAAGT 1266
DB |||||
QY 241 GAAGAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTTCAAGT 300
QY 1267 AAGTCTCTTTATCAAACTCTTATATATAAACAATCAAAACATCAACACGTCGTCTTCG 1326
DB |||||
QY 301 AAGTCTCTTTATCAAACTCTTATATATAAACAATCAAAACATCAACACGTCGTCTTCG 360
QY 1327 TTTTCGATTCTAGATACGATTTTTTTAGTTTCATGTGAATGAACCTCTGTTTTATTACTACTAG 1386
DB |||||
QY 361 TTTTCGATTCTAGATACGATTTTTTTAGTTTCATGTGAATGAACCTCTGTTTTATTACTACTAG 420
QY 1387 GGTGTTTCAATATTTTCGAGAAATTCACGAGGAAACAAAGTTAGTGATTATATTGATGC 1446
DB |||||
QY 421 GGTGTTTCAATATTTTCCGAGAAATTCACGAGGAAACAAAGTTAGTGATTATATTGATGC 480
QY 1447 AGAGTATGAAGTAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 1506
DB |||||
QY 481 AGAGTATGAAGTAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 540
QY 1507 ATATATAAGAAGTTTTTTTTTGGTGAAAAAATATGTATGAGAAAGTTTCATCTTTCATAATA 1566
DB |||||
QY 541 ATATATAAGAAGTTTTTTTTTGGTGAAAAAATATGTATGAGAAAGTTTCATCTTTCATAATA 600
QY 1567 GTGAAAACACTCTCTTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAAACTCTCT 1626
DB |||||
QY 601 GTGAAAACACTCTCTTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAAACTCTCT 660
QY 1627 TTGTCGGATTAGGTTAGGTTTGGACTCAGAATCAAAATACGATTAGCATAAACAAATTTTT 1686
DB |||||
QY 661 TTGTCGGATTAGGTTAGGTTTGGACTCAGAATCAAAATACGATTAGCATAAACAAATTTTT 720
QY 1687 TGGCATGGCAATTTATGTTCTGCAAGGTAAATATACCAATAGAAACATATTTTTTAGGAGTA 1746
DB |||||
QY 721 TGGCATGGCAATTTATGTTCTGCAAGGTAAATATACCAATAGAAACATATTTTTTAGGAGTA 780
QY 1747 GTTAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAATTTCTTTTCTGTGTTT 1806
DB |||||
QY 781 GTTAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAATTTCTTTTCTGTGTTT 840
QY 1807 TTGTTTTTGTGCTGTTTTATAGAACTTTGAATATGTACTTTTTTGTTTTTTTCACCAGTAGA 1866
DB |||||
QY 841 TTGTTTTTGTGCTGTTTTATAGAACTTTGAATATGTACTTTTTTGTTTTTTTCACCAGTAGA 900
QY 1867 TATGTACTATACACATTAAGTAACATGGGTAGTTTATATAGAGAGAGATTGATTTTTTC 1926
DB |||||

Db 901 TATGTACTATACACATAAGTAACATGGGTAGTGTATATAGAGAGAGATTTGATTTTC 960
Qy 1927 GTATATTTCTTTGTTGAAATAAATATGCTGTAATAATTTATTTATTTATTTGACAGA 1986
Db 961 GTATATTTCTTTGTTGAAATAAATATGCTGTAATAATTTATTTATTTATTTGACAGA 1020
Qy 1987 TTTGTTCCACGTTGAGAAGTTTAATTTAGATTAAACAAACAAAAG 2030
Db 1021 TTTGTTCCACGTTGAGAAGTTTAATTTAGATTAAACAAACAAAAG 1064

RESULT 4
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ID AAC49043 standard; DNA; 999 BP.
XX
AC AAC49043;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 59714.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.

XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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PR 09-AUG-1999; 99US-0147493P.

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PR	11-AUG-1999;	99US-0148319P.			
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148565P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	20-AUG-1999;	99US-0149929P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.			
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	27-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.			
PR	31-AUG-1999;	99US-0151438P.			
PR	01-SEP-1999;	99US-0151930P.			
PR	07-SEP-1999;	99US-0152363P.			
PR	10-SEP-1999;	99US-0153070P.			
PR	13-SEP-1999;	99US-0153758P.			
PR	15-SEP-1999;	99US-0154018P.			
PR	16-SEP-1999;	99US-0154039P.			
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PR	05-OCT-1999;	99US-0157753P.			
PR	06-OCT-1999;	99US-0157865P.			
PR	07-OCT-1999;	99US-0158029P.			
PR	08-OCT-1999;	99US-0158232P.			
PR	12-OCT-1999;	99US-0158369P.			
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Query Match 4.7%; Score 95.4; DB 3; Length 999;					
Best Local Similarity 81.0%; Pred. No. 5.5e-07;					
Matches 111; Conservative 0; Mismatches 26; Indels 0; Gaps 0;					
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Db	1	AGAGAGACAATTAATCAGTTTCGTGTGTTTGGAGAAGAGAACAGATCAAAATACGAG	60
QY	1234	GAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTTATCAAACTCTTAATATA	1293
Db	61	GAGAGATCTCTAAAGAGATTTATCGTTTCAAAATTTGTTTCACGTTGAGAGGTTTAATTTAG	120
QY	1294	AACAAATCAAAACATGA	1310
Db	121	ATTAACAACAAAAAGA	137
RESULT 5			
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ID	AAC37034 standard; DNA; 1001 BP.		
XX	AAC37034;		
XX	17-OCT-2000 (first entry)		
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 15944.		
DE	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; ss.		
XX	Arabidopsis thaliana.		
OS	EP1033405-A2.		
XX	06-SEP-2000.		
PD	25-FEB-2000; 2000EP-00301439.		
PF	99US-0121825P.		
XX	99US-0123180P.		
PR	99US-0123548P.		
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PR	99US-0126785P.		
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PR	99US-0128234P.		
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PR	99US-0129845P.		
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PR	99US-0130449P.		
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PR	99US-0131449P.		
PR	99US-0132048P.		
PR	99US-0132484P.		
PR	99US-0132485P.		
PR	99US-0132486P.		
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PR	99US-0132863P.		
PR	99US-0134256P.		
PR	99US-0134218P.		
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PR	99US-0134221P.		
PR	99US-0134370P.		
PR	99US-0134768P.		
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PR	99US-0135124P.		
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PR	99US-0137528P.		
PR	99US-0137502P.		
PR	99US-0137724P.		

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PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
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PR 12-AUG-1999; 99US-0148341P.
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PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
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PR 28-OCT-1999; 99US-0161992P.
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Query Match 4.7%; Score 95.4; DB 3; Length 1001;
Best Local Similarity 81.0%; Pred. No. 5.5e-07;
Matches 111; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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PR	09-AUG-1999;	99US-0147493P.	Db	1	AGAGACAATTAAATCAGTTTCTGTTGTTGGAGAGAGAGAAAGACAGATCAATAACGAGGA	60
PR	09-AUG-1999;	99US-0147935P.	QY	1236	GAGATCTCTAAAGAGATTATCGTTTCAAGTAAGTCTCTTATCAAACTCTTAATATAA	1295
PR	10-AUG-1999;	99US-0148171P.	Db	61	GAGATCTCTAAAGAGATTATCGTTTCAAAATTTGTTCAAGTTGAGAGTTTAAATTTAGAT	120
PR	11-AUG-1999;	99US-0148319P.	QY	1296	CAATCAAAACATGA	1310
PR	12-AUG-1999;	99US-0148341P.	Db	121	TAAACAACAAAGA	135
PR	13-AUG-1999;	99US-0148565P.	QY	1296	CAATCAAAACATGA	1310
PR	13-AUG-1999;	99US-0148684P.	Db	121	TAAACAACAAAGA	135
PR	16-AUG-1999;	99US-0149368P.	QY	1296	CAATCAAAACATGA	1310
PR	17-AUG-1999;	99US-0149175P.	Db	121	TAAACAACAAAGA	135
PR	18-AUG-1999;	99US-0149426P.	QY	1296	CAATCAAAACATGA	1310
PR	20-AUG-1999;	99US-0149722P.	Db	121	TAAACAACAAAGA	135
PR	20-AUG-1999;	99US-0149723P.	QY	1296	CAATCAAAACATGA	1310
PR	20-AUG-1999;	99US-0149929P.	Db	121	TAAACAACAAAGA	135
PR	23-AUG-1999;	99US-0149902P.	QY	1296	CAATCAAAACATGA	1310
PR	23-AUG-1999;	99US-0149930P.	Db	121	TAAACAACAAAGA	135
PR	25-AUG-1999;	99US-0150566P.	QY	1296	CAATCAAAACATGA	1310
PR	26-AUG-1999;	99US-0150884P.	Db	121	TAAACAACAAAGA	135
PR	27-AUG-1999;	99US-0151065P.	QY	1296	CAATCAAAACATGA	1310
PR	27-AUG-1999;	99US-0151066P.	Db	121	TAAACAACAAAGA	135
PR	27-AUG-1999;	99US-0151080P.	QY	1296	CAATCAAAACATGA	1310
PR	30-AUG-1999;	99US-0151303P.	Db	121	TAAACAACAAAGA	135
PR	31-AUG-1999;	99US-0151438P.	QY	1296	CAATCAAAACATGA	1310
PR	01-SEP-1999;	99US-0151930P.	Db	121	TAAACAACAAAGA	135
PR	07-SEP-1999;	99US-0152363P.	QY	1296	CAATCAAAACATGA	1310
PR	10-SEP-1999;	99US-0153070P.	Db	121	TAAACAACAAAGA	135
PR	13-SEP-1999;	99US-0153758P.	QY	1296	CAATCAAAACATGA	1310
PR	15-SEP-1999;	99US-0154018P.	Db	121	TAAACAACAAAGA	135
PR	16-SEP-1999;	99US-0154039P.	QY	1296	CAATCAAAACATGA	1310
PR	20-SEP-1999;	99US-0154779P.	Db	121	TAAACAACAAAGA	135
PR	22-SEP-1999;	99US-0155139P.	QY	1296	CAATCAAAACATGA	1310
PR	23-SEP-1999;	99US-0155486P.	Db	121	TAAACAACAAAGA	135
PR	24-SEP-1999;	99US-0155653P.	QY	1296	CAATCAAAACATGA	1310
PR	28-SEP-1999;	99US-0156458P.	Db	121	TAAACAACAAAGA	135
PR	29-SEP-1999;	99US-0156596P.	QY	1296	CAATCAAAACATGA	1310
PR	04-OCT-1999;	99US-0157117P.	Db	121	TAAACAACAAAGA	135
PR	05-OCT-1999;	99US-0157753P.	QY	1296	CAATCAAAACATGA	1310
PR	06-OCT-1999;	99US-0157863P.	Db	121	TAAACAACAAAGA	135
PR	07-OCT-1999;	99US-0158029P.	QY	1296	CAATCAAAACATGA	1310
PR	08-OCT-1999;	99US-0158232P.	Db	121	TAAACAACAAAGA	135
PR	12-OCT-1999;	99US-0158369P.	QY	1296	CAATCAAAACATGA	1310
PR	13-OCT-1999;	99US-0159293P.	Db	121	TAAACAACAAAGA	135
PR	13-OCT-1999;	99US-0159294P.	QY	1296	CAATCAAAACATGA	1310
PR	13-OCT-1999;	99US-0159295P.	Db	121	TAAACAACAAAGA	135
PR	14-OCT-1999;	99US-0159330P.	QY	1296	CAATCAAAACATGA	1310
PR	14-OCT-1999;	99US-0159331P.	Db	121	TAAACAACAAAGA	135
PR	14-OCT-1999;	99US-0159637P.	QY	1296	CAATCAAAACATGA	1310
PR	14-OCT-1999;	99US-0159638P.	Db	121	TAAACAACAAAGA	135
PR	18-OCT-1999;	99US-0159584P.	QY	1296	CAATCAAAACATGA	1310
PR	21-OCT-1999;	99US-0160741P.	Db	121	TAAACAACAAAGA	135
PR	21-OCT-1999;	99US-0160767P.	QY	1296	CAATCAAAACATGA	1310
PR	21-OCT-1999;	99US-0160768P.	Db	121	TAAACAACAAAGA	135
PR	21-OCT-1999;	99US-0160770P.	QY	1296	CAATCAAAACATGA	1310
PR	21-OCT-1999;	99US-0160814P.	Db	121	TAAACAACAAAGA	135
PR	21-OCT-1999;	99US-0160815P.	QY	1296	CAATCAAAACATGA	1310
PR	22-OCT-1999;	99US-0160980P.	Db	121	TAAACAACAAAGA	135
PR	22-OCT-1999;	99US-0160981P.	QY	1296	CAATCAAAACATGA	1310
PR	22-OCT-1999;	99US-0160989P.	Db	121	TAAACAACAAAGA	135
PR	25-OCT-1999;	99US-0161404P.	QY	1296	CAATCAAAACATGA	1310
PR	25-OCT-1999;	99US-0161405P.	Db	121	TAAACAACAAAGA	135
PR	25-OCT-1999;	99US-0161406P.	QY	1296	CAATCAAAACATGA	1310
PR	26-OCT-1999;	99US-0161359P.	Db	121	TAAACAACAAAGA	135
PR	26-OCT-1999;	99US-0161360P.	QY	1296	CAATCAAAACATGA	1310
PR	26-OCT-1999;	99US-0161361P.	Db	121	TAAACAACAAAGA	135
PR	28-OCT-1999;	99US-0161920P.	QY	1296	CAATCAAAACATGA	1310
PR	28-OCT-1999;	99US-0161920P.	Db	121	TAAACAACAAAGA	135
PR	28-OCT-1999;	99US-0161922P.	QY	1296	CAATCAAAACATGA	1310
PR	28-OCT-1999;	99US-0161933P.	Db	121	TAAACAACAAAGA	135
PR	29-OCT-1999;	99US-0162142P.	QY	1296	CAATCAAAACATGA	1310
Query Match			4.6%; Score 93.4; DB 3; Length 495;			
Best Local Similarity			80.7%; Pred. No. 1.1e-06;			
Matches 109; Conservative			0; Mismatches 26; Indels 0; Gaps 0;			

RESULT 8
ACA64845
ID ACA64845 standard; DNA; 115218 BP.
XX
XX
AC ACA64845;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human HNRNP GP43 DNA corresponding to AL034397.
XX
XX Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW immunosuppressive; gene therapy; etioloical pathogenicity; ds.
XX
XX Homo sapiens.
OS
XX
XX DE10127572-A1.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2001; 2001DE-01027572.
XX
XX 30-MAY-2001; 2001DE-01027572.
XX
XX (PATH-) PATHOARRAY GMBH.
XX
XX Haeupl T, Ungethuem U, Blaess S;
XX
XX WPI; 2003-240797/24.
XX
XX Reagents for diagnosis, study and therapy of chronic inflammatory joint
PT and other diseases, comprises any of many specified genes or derived
PT proteins.
XX
XX Claim 1; Page; 12pp; German.
XX
XX This invention describes a novel reagent for diagnosis, molecular
CC definition and therapy of chronic inflammatory joint diseases, and other
CC inflammatory disorders, infective or tumour diseases in humans. The
CC products of the invention have antiinflammatory, cytostatic,
CC antiarthritic, antirheumatic and immunosuppressive activity and can be
CC used for gene therapy. The reagent of the invention and any proteins and
CC antibodies derived from it, are used (i) for analysing tissue and blood
CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC chronic joint diseases, on the basis of molecular characterisation, and
CC determining the etiological pathogenicity principle of as yet
CC uncharacterised inflammatory diseases, also monitoring progression and/or
CC treatment of disease, and optimisation of therapy and (iii) for
CC developing treatments for inflammatory diseases, particularly of joints,
CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides
XX used in the method of the invention
XX
XX Sequence 115218 BP; 35618 A; 23477 C; 22286 G; 33837 T; 0 U; 0 Other;
SQ
Query Match 4.4%; Score 88.4; DB 8; Length 115218;
Best Local Similarity 46.5%; Pred No. 1.1e-05;
Matches 319; Conservative 0; Mismatches 366; Indels 1; Gaps 1;
Qy 28 ATACTTCTCTTTCTATTTTATTTGATTTAGAAAATCATATTCATTACAAAAGGAAAA 87
Db 16900 AT 16959
Qy 88 AAAAAATATTTTGTATCTTAAAGTTATACATTACA-ATTTCACACTTCAGTTGG 146
Db 16960 AAT 17019
Qy 147 TAGTATTAATTTATCTATTTTATCAAGTTTGGTTTGGAGAAAATGTATCTTTTCATA 206
Db 17020 TATTAT 17079
Qy 207 TAAAAAATATATAGATCTTCAAGAAACGTAATCGGTTTTCAACTATTTTATCGTTGA 266
Db 17080 TATTATATATATATATATATTTTATATATATATATATATATATATATATATATATAT 17139

Qy 267 CACTACTTTGACTTATCAAAAAGAGTTCAAAAATAGAAAAATAGAAATCGAATCACACGTTT 326
Db 17140 GATATATTATATTATTA 17199
Qy 327 CAGGTGAAGAGGATTTGGTATTTGGTCGACATTTTAAAGAGTTGTTGTTTTTTTTTCC 386
Db 17200 TATTATATGATA 17259
Qy 387 AATCTGCATGTTTTCGTTCCGTTGAACCAAAATTCACACTTTGTATAAACCGAATAGT 446
Db 17260 TAT 17319
Qy 447 AATATACTAGACGTCGCCCAATACCAAAAATATAAATTTAAACTCAATTCACAAATGNAAT 506
Db 17320 ATATAATAAATATATATAATATAATATAATATAATATAATATAATATAATATAATAT 17379
Qy 507 CTCACCATATATCAT 566
Db 17380 ATATAACATA 17439
Qy 567 ATAATCAATATCCAACTCAACGATAATCAAAAGCTAATAATAGATCAATGAAATCAAAAT 626
Db 17440 ATATAAT 17499
Qy 627 AACTAAAACATAGTAAT 686
Db 17500 ATA 17559
Qy 687 ATGAAAATATGAAT 712
Db 17560 TTA 17595
RESULT 9
AAC52118
ID AAC52118 standard; DNA; 515 BP.
XX
AC AAC52118;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70414.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 28-APR-1999; 99US-0130891P.
XX 30-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.

PR	04-MAY-1999;	99US-0132484P.
PR	05-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	07-MAY-1999;	99US-0132487P.
PR	11-MAY-1999;	99US-0132863P.
PR	11-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134221P.
PR	14-MAY-1999;	99US-0134370P.
PR	18-MAY-1999;	99US-0134768P.
PR	19-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	10-JUN-1999;	99US-0138847P.
PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.
PR	16-JUN-1999;	99US-0139453P.
PR	17-JUN-1999;	99US-0139492P.
PR	18-JUN-1999;	99US-0139454P.
PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139456P.
PR	18-JUN-1999;	99US-0139457P.
PR	18-JUN-1999;	99US-0139458P.
PR	18-JUN-1999;	99US-0139460P.
PR	18-JUN-1999;	99US-0139461P.
PR	18-JUN-1999;	99US-0139462P.
PR	18-JUN-1999;	99US-0139463P.
PR	18-JUN-1999;	99US-0139750P.
PR	18-JUN-1999;	99US-0139763P.
PR	21-JUN-1999;	99US-0139817P.
PR	22-JUN-1999;	99US-0139899P.
PR	23-JUN-1999;	99US-0140353P.
PR	23-JUN-1999;	99US-0140354P.
PR	24-JUN-1999;	99US-0140695P.
PR	28-JUN-1999;	99US-0140823P.
PR	29-JUN-1999;	99US-0140991P.
PR	30-JUN-1999;	99US-0141287P.
PR	01-JUL-1999;	99US-0141842P.
PR	01-JUL-1999;	99US-0142154P.
PR	02-JUL-1999;	99US-0142055P.
PR	06-JUL-1999;	99US-0142390P.
PR	08-JUL-1999;	99US-0142803P.
PR	09-JUL-1999;	99US-0142920P.
PR	12-JUL-1999;	99US-0142977P.
PR	13-JUL-1999;	99US-0143542P.
PR	14-JUL-1999;	99US-0143624P.
PR	15-JUL-1999;	99US-0144005P.
PR	16-JUL-1999;	99US-0144085P.
PR	16-JUL-1999;	99US-0144086P.
PR	18-JUL-1999;	99US-0144325P.
PR	19-JUL-1999;	99US-0144331P.
PR	19-JUL-1999;	99US-0144332P.
PR	19-JUL-1999;	99US-0144333P.
PR	19-JUL-1999;	99US-0144334P.
PR	19-JUL-1999;	99US-0144335P.
PR	20-JUL-1999;	99US-0144352P.
PR	20-JUL-1999;	99US-0144632P.
PR	20-JUL-1999;	99US-0144684P.
PR	21-JUL-1999;	99US-0144814P.
PR	21-JUL-1999;	99US-0145086P.
PR	21-JUL-1999;	99US-0145088P.
PR	22-JUL-1999;	99US-0145085P.
PR	22-JUL-1999;	99US-0145087P.
PR	22-JUL-1999;	99US-0145089P.
PR	22-JUL-1999;	99US-0145192P.
PR	23-JUL-1999;	99US-0145145P.
PR	23-JUL-1999;	99US-0145218P.
PR	23-JUL-1999;	99US-0145224P.
PR	26-JUL-1999;	99US-0145276P.
PR	27-JUL-1999;	99US-0145913P.
PR	27-JUL-1999;	99US-0145918P.
PR	27-JUL-1999;	99US-0145919P.
PR	28-JUL-1999;	99US-0145951P.
PR	02-AUG-1999;	99US-0146386P.
PR	02-AUG-1999;	99US-0146388P.
PR	02-AUG-1999;	99US-0146389P.
PR	03-AUG-1999;	99US-0147038P.
PR	04-AUG-1999;	99US-0147204P.
PR	04-AUG-1999;	99US-0147302P.
PR	05-AUG-1999;	99US-0147192P.
PR	05-AUG-1999;	99US-0147260P.
PR	06-AUG-1999;	99US-0147303P.
PR	06-AUG-1999;	99US-0147416P.
PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
PR	10-AUG-1999;	99US-0148171P.
PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
PR	16-AUG-1999;	99US-0149368P.
PR	17-AUG-1999;	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.
PR	20-AUG-1999;	99US-0149723P.
PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149902P.
PR	23-AUG-1999;	99US-0149910P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158212P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159337P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.


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PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161040P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.3%; Score 87.4; DB 3; Length 515;
Best Local Similarity 79.8%; Pred. No. 1.2e-05;
Matches 103; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1182 AATTAATCAGTTTCGTGTGTTGGAGAGAGAGAGAGAGATCAATCAACGAGAGATC 1241
Db 2 AATTAATCAGTTTCGTGTGTTGGAGAGAGAGAGAGAGATCAATCAACGAGAGATC 61

QY 1242 TCTAAAGAGATTTATCGTTTCAAGTAAGTCCTTTATCAAACTCTTAATATAACAAATC 1301
Db 62 TCTAAAGAGATTTATCGTTTCAAAATTTGTCACGTTGAGAGATTTAATTTAGATTAACA 121

QY 1302 AAAACATGA 1310
Db 122 ACAAAAGA 130

RESULT 10
ABZ10100/c
ID ABZ10100 standard; DNA; 8056 BP.
XX
AC ABZ10100;
XX
XX 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
XX WO200277272-A2.
XX
PD 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-EP003401.
XX
XX 26-MAR-2001; 2001US-0278333P.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Quetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwobe I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 28; SEQ ID NO 240; 117pp; English.
PS
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XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB211118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Query Match 4.1%; Score 82.8; DB 8; Length 8056;
Best Local Similarity 46.2%; Pred. No. 8.1e-05;
Matches 317; Conservative 0; Mismatches 362; Indels 7; Gaps 1;

QY 36 TCTTTCTATTTTATTTGATTTAGAAAAATCATATTCTTACAAAAGGAAAAAATA 95
Db 2063 TTTTAAAAAATAAAAAATATTTAAAAATATATTTTATTTTAAAAATTTTAA 2004

QY 96 ATTTTGTATCTCTAAAGTTATACTTTTCCACACTTCAGTTGCTAGTATTAA 155
Db 2003 TTTAAATTTTAAATAAAAAATTAATTAATATTTTATTTTAAAAATATATATTTTAT 1944

QY 156 TTTATCTATTTTATCAAGTTTGGTTTGTAGAAAAATGTATCTTTTCATATAAAAAATA 215
Db 1943 TTATATTATTAATTTAATTTATTTTATTTTATTAATAATTTTATTTTATATAAAAAA 1884

QY 216 TATAGATCTTCAAAAGAACTGAATGGTGTTCACACTATTTTATCGTTTGACACTCTTT 275
Db 1883 TAAAAATAATTAATTAATTAATTTTATTTTATTTTATTTTAAAAACGAAATTT 1824

QY 276 GACTTATCAAAAGAGTTTCAAAATAGAAAAATAGAAATCGAATCACAGTTTCAGTGAAG 335
Db 1823 TATTTTATTTAATTTAAAAATATAAATTAACGTAATTTTATTTTATTTTAAATTTAA 1764

QY 336 AGGATTTGATATTGGTCGACATTTTAAAGAGTTGTTTGTGTTTTCCTCAATCTGCAT 395
Db 1763 AATTTTATTTTAAATTTTAAATTTTAAATTTAATTAATAATATAATATATATATATATA 1704

QY 396 GGTTTTTCGTTCCGTGGAACCAAAATTCACACTTTTGTATAAACCGAAATAGTAATATACTA 455
Db 1703 TTAATTTTATAATTTTAAATAAAAAATAAATTTTATCGTATTAATTAATAATAATTTT 1644

QY 456 GACGTACGCCAATACCAAAAAATAAAATTAACACTCAATTCACAAATTCGAATCTACACCAT 515
Db 1643 TAAATTTACGATTCGTTTATTTTCGATTTTAAAAATATTAATAATTTAATAATAATAATA 1584

QY 516 ATCA-----TGCATATATATACGCAACCTFAGATAATCAATGAAATTTAATCGAGAT 568
Db 1583 AATATTAAATTTAAATAATAATTTTAAAAAATAATTTTATTTTAAAAATTTTTCACG 1524

QY 569 AATCAATATCCAACCTCAACGATAATCAAAAGCCTAATAATAGATCAATGAAATCAAAATA 628
Db 1523 TATTTATATTTTATATTTATATAATATTAATTAATTAATTAATTTTAAATATAATTT 1464

QY 629 CTAACATAGTAATATACATTTGTTGTTTAAACAGAAATATATACATTAATAGATAT 688
Db 1463 ATTAATAAATAATTTTATTTTATTTTATTTTAAAAAATAAATAAATAAATAAATAA 1404
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KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX Homo sapiens.
 OS WO200200928-A2.
 FN 03-JAN-2002.
 PD 02-JUL-2001; 2001WO-EP007537.
 PF 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2002-130909/17.
 DR Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.
 PS The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 XX ds.
 SQ Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 U; 0 Other;
 Query Match 3.9%; Score 78.8; DB 6; Length 15548;
 Best Local Similarity 46.6%; Pred. No. 0.00039;
 Matches 324; Conservative 0; Mismatches 367; Indels 5; Gaps 2;
 QY 62 AAATCATATTCATTACAAAAGGAAAAAATAATTTTTGTATCCTAAAGTTTATAACT 121
 DB 12299 ATATACATATATATATATATACATATATATATATACATATATATATATATATATATAT 12240
 QY 122 TACATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAAGTTTGGT 181
 DB 12239 AACATATATATATACATATATATATATACATATATATATATATATATATATATATAT 12180
 QY 182 TTTAGGAAAAATGTATCTTTTCATATAAAAATATATAGATCTTCAAGAACTGAATTG 241
 DB 12179 TATATATACAT 12120
 QY 242 GGTTCCTCACTTTTATGTTTGCACCTTCTTCACTTATCAAAAGAGTTTCAAAATAG 301
 DB 12119 CATATAAAATATACAT 12060
 QY 302 AAAAATAGATCGAATCACACAGCTTTTCAGTGTGAAGGGATTTGATTTGGTCGACATTTT 361
 DB 12059 AATAACATATAAAATACATATAAAATATAAAATATAAAATATAAAATATAATATATATAT 12000
 QY 362 AAAGAGTTGTTTGTGTTTTTTTCCAACTGCATGGTTTTTCGTTCCGTTGACCAAAATT 421
 DB 11999 AAAAAATAAAT 11940
 QY 422 CAACACTTTGTATAACCGAATAGTAATATCTAGACGGTACGCCAATCAAAATAAA 481
 DB 11939 TAAAAATAAAT 11880
 QY 482 TTAAACTCAATTCACAAATTTGAATCTCACCATATCATGCATATATATATATATATATATAT 541
 DB 11879 AT 11820

QY 542 AATA-ATCAATGAAATTTTAAATCCAGGATAATCAATATCCAACTCAACGATAATCAAAAGC 600
 DB 11819 AATATAAAATATAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 11760
 QY 601 CTAATAATAGATCAATGAAATCAAAATCAATCAATCAATCAATCAATCAATCAATCAATCA 660
 DB 11759 AATAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 11700
 QY 661 AACAGAATAATATATACATTATAATAGTATGAAATATGAATATATATATATATATATATAT 720
 DB 11699 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 11644
 QY 721 TATGTTACACTACAGATCCACATCCCAATTAACA 756
 DB 11643 AATATAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 11608
 RESULT 13
 ABL32426/C
 ID ABL32426 standard; DNA; 9810 BP.
 XX
 AC ABL32426;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 399.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cytosatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX WO200200928-A2.
 FN 03-JAN-2002.
 PD 02-JUL-2001; 2001WO-EP007537.
 PF 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2002-130909/17.
 DR Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX Claim 1; SEQ ID NO 399; 32pp + Sequence Listing; German.
 PS The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 XX ds.
 SQ Sequence 9810 BP; 2770 A; 79 C; 1978 G; 4983 T; 0 U; 0 Other;
 Query Match 3.7%; Score 76; DB 6; Length 9810;
 Best Local Similarity 45.3%; Pred. No. 0.0011;

Qy 750 ATTACAAAT 758
Db 5196 TATATATAT 5188

Search completed: October 23, 2005, 22:24:28
Job time : 1099 secs

Result No.	Score	Query Match	Length	DB	ID	Description	Sequence 22, Appl
1	72.4	3.6	1141	4	US-09-806-708B-22	Sequence 22, Appl	Sequence 22, Appl
2	72.2	3.6	18773	4	US-09-949-016-14164	Sequence 14164, A	Sequence 14164, A
3	71.8	3.5	640681	4	US-09-790-988-1	Sequence 1, Appl	Sequence 1, Appl
c	70.8	3.5	1141	4	US-09-806-708B-22	Sequence 22, Appl	Sequence 22, Appl
5	69.8	3.4	205044	4	US-09-949-016-15851	Sequence 15851, A	Sequence 15851, A
6	69.8	3.4	205044	4	US-09-949-016-15852	Sequence 15852, A	Sequence 15852, A
7	69.8	3.4	205044	4	US-09-949-016-15853	Sequence 15853, A	Sequence 15853, A
8	69.8	3.4	223471	4	US-09-949-016-12387	Sequence 12387, A	Sequence 12387, A
9	69.8	3.4	223471	4	US-09-949-016-13724	Sequence 13724, A	Sequence 13724, A
10	69.8	3.4	223471	4	US-09-949-016-13725	Sequence 13725, A	Sequence 13725, A
11	68.8	3.4	29717	4	US-09-949-016-16284	Sequence 16284, A	Sequence 16284, A
12	68.8	3.4	60376	4	US-09-949-016-14243	Sequence 14243, A	Sequence 14243, A
13	67.8	3.3	134987	4	US-09-949-016-15348	Sequence 15348, A	Sequence 15348, A
14	67.8	3.3	134987	4	US-09-949-016-15349	Sequence 15349, A	Sequence 15349, A
15	67.8	3.3	134987	4	US-09-949-016-15350	Sequence 15350, A	Sequence 15350, A
16	67.8	3.3	134987	4	US-09-949-016-15507	Sequence 15507, A	Sequence 15507, A
17	67.8	3.3	134987	4	US-09-949-016-15508	Sequence 15508, A	Sequence 15508, A
18	67.8	3.3	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
c	66	3.3	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
19	66	3.3	134987	4	US-09-949-016-14164	Sequence 14164, A	Sequence 14164, A
20	65.2	3.2	114139	4	US-09-949-016-16536	Sequence 16536, A	Sequence 16536, A
21	65	3.2	30820	4	US-09-949-016-17145	Sequence 17145, A	Sequence 17145, A
c	65	3.2	134987	4	US-09-949-016-15348	Sequence 15348, A	Sequence 15348, A
22	65	3.2	134987	4	US-09-949-016-15349	Sequence 15349, A	Sequence 15349, A
c	65	3.2	134987	4	US-09-949-016-15350	Sequence 15350, A	Sequence 15350, A
23	65	3.2	134987	4	US-09-949-016-15350	Sequence 15350, A	Sequence 15350, A
c	65	3.2	134987	4	US-09-949-016-15507	Sequence 15507, A	Sequence 15507, A
24	65	3.2	134987	4	US-09-949-016-15508	Sequence 15508, A	Sequence 15508, A
c	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
25	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
c	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
26	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
c	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
27	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A
c	65	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A	Sequence 15509, A

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Db 479 WNNCYWKSMTNGKSHRBAAYVYTWYMWRRYAHANNNNNDYWKWACTWYKYBVCWKWN 538
Qy 953 TCACATGCTCTTCATGGTGACGTAACAAGACTTATTTTCGGGTTCAATTTGGTTTAACCTA 1012
Db 539 NYAAWYTKSWNYTSRYRKYRKTNNNSWRSDTRSGMRANNYARABHYGYKWNTRWBSH 598
Qy 1013 TTGAGATTGCTTAACCGGAAACAGAACGGTTATGACGCCCAACGAGCGGCAAGGGGTAA 1072
Db 599 TWBHRAGAHHYMBMYBAKCHWKAWYKAKKYGAGGSGNNNNNNNNNNNNNNNNNNATCA 658
Qy 1073 AACGAGAAAGAGGGGATCGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGGTTTCAC 1132
Db 659 RDDYAA-----SRWYAMANAkWYKBAANNAYYTHANNWGCWNNATDTRRTWKNN 712
Qy 1133 GATAAGTCTGTCTATATGACGCGAAAGGTTTCTTAAATTCAGAGACAAATTAATCAGT 1192
Db 713 NNNNAGTWKNNNNNNNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAK 772
Qy 1193 TTCGTGTTGGAGAGAGAGAACAGATCAATACGAGGAGAGATCTCTAAAGAGAT 1252
Db 773 NNGAYTKYTTNNNTYRGVVNTAARDGWANNNNNNNNNNNNNNNNNNNNNGWSMDMWVWYANY 832
Qy 1253 TTATCGTTTCAAGTAAGTCTCTTATCAAACTCTTAATATAAAACAAATCAAAACATCAAC 1312
Db 833 GTNNNNNNNNNAWAWTNKWWYTTDDRWBAYTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 892
Qy 1313 ACGTGCTGCTTCGTTTCGATTCAGATACAGATTTTTCGATTCGATTCGATTCGATTCGAT 1372
Db 893 DAWMKWDATKNNNATYNNRGTAWRTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 952
Qy 1373 TTATTTACTACTAGGTTGTTCAATATTTTCCGAGAAATACGAGAGGACAAAGTTAGT 1432
Db 953 VCKATKTKGCMNCTTCRKYKNNCTWYTWMTTTRTTWYAAATRWKNNNNATGSMTRCNAT 1012
Qy 1433 GATTATATTGATGACAGATGAGTGAAGTAAATATATATACATAAATCAATGTTTTCCTCAAGC 1492
Db 1013 GWKNNYWTGKTRWYATRWATRWKAWKWKVMTGSMNNSYARWAYKTRAYKGWYNAC 1072
Qy 1493 ATCTACGTTGAAATATATATA 1513
Db 1073 AWRWRGKATCYMTDNAWTA 1093

RESULT 2
US-09-949-016-14164
; Sequence 14164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14164
; LENGTH: 18773
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14164

Query Match 3.6%; Score 72.2; DB 4; Length 18773;
Best Local Similarity 46.5%; Pred. No. 2.9e-05;
Matches 308; Conservative 0; Mismatches 348; Indels 7; Gaps 2;

Qy 49 TATTGATTAGAAATCATATTTCATACAAAGGAAAAAATAATTTTGTATCC 108
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Db 17714 TATATATATAATCTGTAATAATATAATATATATATATATATATATATATATATGT 17773
Qy 109 TAAAGTTATAACCTTACAAATTTTCCACACTTCAGTTGGTAGTATTAATTTATCTATTTT 168
Db 17774 AATATATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 17833
Qy 169 ATCAAGTTTGGTTTGGGAAATCTATCTTTTCATATAAAAAATATATAGATCTTCAA 228
Db 17834 TATAATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 17893
Qy 229 AGAAATCGAATTTGGGTTTTCACACTTTTATCGTTTGACACTTCTGACCTTATCAAAA 288
Db 17894 ATATATGATATATATTTTATATATATATATATATATATATATATATATATATGA 17953
Qy 289 GAGTTCAAAATAGAAAAATAGAAATCGAAATCACAGTTTCAGTGTAGAGGATTTGATAT 348
Db 17954 AATTTATATATACTATATATATAATAATAATAATAATAATAATAATAATAATAATA 18013
Qy 349 TCGTCGACATTTTAAAGAGTTGTTTGTGTTTTCCTCAATCTGCATGTTTTCGTTCC 408
Db 18014 TATTATATATATATATATATATATATATATATATATATATATATATATATATACAA 18073
Qy 409 GTTGAACCAAAATTCACACTTTTGTATAAAACCGAATAGTAACTACTAGACGTACGCCAAT 468
Db 18074 TATGATATATAATAATTTATATATATATATATATATATATATATATATATATA-TAAAT 18132
Qy 469 ACCAAAAATAAATTTAAACTCAATTCACAAATTTGAATCTACACCATATCATCATATAT 528
Db 18133 ATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 18186
Qy 529 ATCAGCAACCTAGAAATCAATGAAATTTAATCGAGGAGTAACTCAATATCCAACTCAACG 588
Db 18187 TTATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 18246
Qy 589 ATATCAAAAGCCCTAATAATAGATCAATGAAATCAAAATCAAACTAAACATAGTAAATACAT 648
Db 18247 TAAATAATAACATATATTTTATATAAGAATAATATATAATAATCATATATATTTTATA 18306
Qy 649 TGATTTGTGTTAAACAGATAATAATATACATTTAATAGTATGAAAAATATGAATAATAAG 708
Db 18307 TAGAATATTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 18366
Qy 709 ATA 711
Db 18367 ATA 18369

RESULT 3
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 3.5%; Score 71.8; DB 4; Length 640681;
Best Local Similarity 47.8%; Pred. No. 7.6e-05;
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15851
; LENGTH: 205044
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851
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Query Match 3.4%; Score 69.8; DB 4; Length 205044;
Best Local Similarity 46.3%; Pred. No. 0.00015;
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;

QY 72 CATTACAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATAAATCAATTTTC 131
DB 200437 CAAAATAAATCAAAATATATTTAAATATATATACATTTATAGGTATATCAAT 200496

QY 132 CACACTTCAGTTGGTAGTATTAATTTTATCTATTTTATCAAAAGTTGGTTTAGGAAA 191
DB 200497 TTTATCAATATATTTAAATATAAATATATTTATATATTTTAAATATAAATATA 200556

QY 192 ATGTATCTTTTCATATAAAAAATATAGATCTTCAAGAAACTGAATTCGTTTCAAC 251
DB 200557 ATATATTTATATATATTTAAATATAAATATATATAAATAATATTTTATATAT 200615

QY 252 TATTTTATCGTTTGACACTCTTGACTTATCAAAAAAGAGTTCAAAATAGAAAAATAGAA 311
DB 200616 -----TATAAATATATAAATATATTTTAAATATAAATATAAATATAA 200670

QY 312 TCGAATCACAGTTTCAGTGTAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTGT 371
DB 200671 TTTATATATATTTTAAATATAAATATAAATAATATTTTATATATATTTTAAATA-TAAA 200729

QY 372 TTTGTTTTTTTCCCAATCTGCATGGTTTTTCGTTCCGTTGACCAAAATTCACACTTTG 431
DB 200730 TATATAAATATATTTTATATATATTTTAAATATAAATATAAATATAAATATAA 200789

QY 432 TATAAACCGAATAGTATACTAGAGGTACGCCAATACCAAAAAATAAATTTAAACCTCA 491
DB 200849 TTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAAATATAA 200909

QY 552 GAAATTTTAAATCGAGGATAATCAATATCCAACTCAACGATATCAAAAGCCTTAATAAGA 611
DB 200910 ATATTTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAA 200969

QY 612 TCAATGAAATCAAAATCAACATAGTAAATATATATTTTAAATATAAATATAAATAA 671
DB 200970 ATATATTTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAA 201029

QY 672 ATACATTTAATAGTATGAAAAATAGTAATATAGATAGAGAGCGGCTATATGTTACAA 730
DB 201030 ATATATATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAA 201088
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RESULT 6
US-09-949-016-15852
; Sequence 15852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15852
; LENGTH: 205044
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852
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Query Match 3.4%; Score 69.8; DB 4; Length 205044;
Best Local Similarity 46.3%; Pred. No. 0.00015;
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;

QY 72 CATTACAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATAAATCAATTTTC 131
DB 200437 CAAAATAAATCAAAATATATTTAAATATATATATATATATATATATATATAT 200496

QY 132 CACACTTCAGTTGGTAGTATTAATTTTATCTATTTTATCAAAAGTTGGTTTAGGAAA 191
DB 200497 TTTATCAATATATTTAAATATAAATATATTTATATATTTTAAATATAAATAA 200556

QY 192 ATGTATCTTTTCATATAAAAAATATAGATCTTCAAGAAACTGAATTCGTTTCAAC 251
DB 200557 ATATATTTATATATATTTTAAATATAAATATATATAAATAATATTTTATATAT 200615

QY 252 TATTTTATCGTTTGACACTCTTGACTTATCAAAAAAGAGTTCAAAATAGAAAAATAGAA 311
DB 200616 -----TATAAATATAAATAATATTTTAAATATAAATATAAATAAATAA 200670

QY 312 TCGAATCACAGTTTCAGTGTAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTGT 371
DB 200671 TTTATATATATTTTAAATATAAATATAAATAATATTTTATATATATTTTAAATA-TAAA 200729

QY 372 TTTGTTTTTTTCCCAATCTGCATGGTTTTTCGTTCCGTTGACCAAAATTCACACTTTG 431
DB 200730 TATATAAATATATTTTATATATATTTTAAATATAAATATAAATATAAATATAA 200789

QY 432 TATAAACCGAATAGTATACTAGAGGTACGCCAATACCAAAAAATAAATTTAAACCTCA 491
DB 200790 TTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAAATAA 200849

QY 492 ATTCACAAATGGAATCTACACCATATCATGCATATATATCAAGCAACCTAGAAATCAAT 551
DB 200850 ATTTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAAATAA 200909

QY 552 GAAATTTTAAATCGAGGATAATCAATATCCAACTCAACGATATCAAAAGCCTTAATAAGA 611
DB 200910 ATATTTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAA 200969

QY 612 TCAATGAAATCAAAATCAACATAGTAAATATATATTTTAAATATAAATATAAATAA 671
DB 200970 ATATATTTTAAATATAAATATAAATAATATATATTTTAAATATAAATATAAATAA 201029

QY 672 ATACATTTAATAGTATGAAAAATAGTAATATAGATAGAGAGCGGCTATATGTTACAA 730
DB 201030 ATATATATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAA 201088
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Db 171217 TTTAAATATAAATATAAATATATATATTTTAAATATAAATATATAAATATATAT 171276
Qy 492 ATTCACAAATGAACTACACCATATCATGCAATATATATACAGCAACCTAGAAATCAAT 551
Db 171277 ATTTTAAATATAAATATAAATATATATATTTTAAATATAAATATATAAATATAT 171336
Qy 552 GAAATTTAATCGAGGATAATCAATATCAACTCAACGATATCAAAAGCCCTAAATAATAGA 611
Db 171337 ATATTTTAAATATAAATATAAATATATATATTTTAAATATAAATATATAAATAT 171396
Qy 612 TCAATGAAATCAAATAACATAGTAATATATATATATTTTAAATATAAATATATAAATAT 671
Db 171397 ATATATTTTAAATATAAATATAAATATATATATTTTAAATATAAATATATAAATAT 171456
Qy 672 ATACATTTAATAGTAGTAAATATGAATATATAATGAGTAAGAGCGGTATATGTACAA 730
Db 171457 ATATATATTTTAAATATAAATATATAAATATATATATTTTAAATATAAATATATAA 171515

RESULT 11

US-09-949-016-16284
; Sequence 16284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16284
; LENGTH: 29717
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(29717)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16284

Query Match 3.4%; Score 68.8; DB 4; Length 29717;
Best Local Similarity 47.0%; Pred. No. 0.00016;
Matches 280; Conservative 0; Mismatches 312; Indels 4; Gaps 2;
Qy 1436 TATATGTGACAGATGTAAGTAATATATACATAAAATCATGTTTGTCTCAAGCATC 1495
Db 15339 TATTTATATATATTTTATATATTTATATATATTTATATATTTATATATATTTATA 15398
Qy 1496 TACGTTGAAATATATATAAGAGTTTTTTTTTGGTGAAAAAATATGATGAGAGTTTCAT 1555
Db 15399 TATATTTATATTTTATATATATTTTATATATTTTATTTATTTATATATTTTATATATA 15458
Qy 1556 CTTTCATAATAGTGAACAACTCTCTTCATACACCAAAAAAATTTGAAAAAATTAG 1615
Db 15459 TATTTTATATATTTTATATATATTTTATATATTTTATATATATTTTATATATTTTA 15518
Qy 1616 TCAAACTCTCTTGTCCGATTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCAT 1675
Db 15519 TATATATTTTATATGATAT-ATTTTATATATTTTATATATTTTATATACATTTCAAT 15577
Qy 1676 AACAAATTTTTGGCATGGCAATTTATGTCGCGGTAAAAATATACCAATAGAAACATAT 1735
Db 15578 ATATTTTATATATTTTATATACATATTCATATATATTTTTTATATATTTTATATACATAT 15637

Qy 1736 TTTTGGAGTAGTTAAGATTATGATTCGAAGAAATACATTTACGATAAGCATAAAATTTTC 1795
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Qy 1796 TTTTGTCTTCTTGGTTTTTGTCTGTTTTATAGAACATTTGAATATGTAATTTTGTGTTTTT 1855
Db 15698 ATATATTTTATTTATATATATTTTATATATTTTATATATTTTATATATTTTATATATAT 15757
Qy 1856 TCACCAGTAGATATGT---ACTATACACACATAGTAAGTAACATGGGTAGTTTATATAGAGAG 1912
Db 15758 TTATTTTATATATATTTTATATATTTTATATATTTTATATATTTTATATATATATTT 15817
Qy 1913 AGATTTGATTTTTCGTAATATTTCTTTTGGTGAATAAATAATGTAATGTAATAATTTTGT 1972
Db 15818 ATATATTTTATTTATATATTTTACATATATTTTATATATTTTATATATTTTATATATTT 15877
Qy 1973 ATTAATTTTGACAGATTTTGTTCACGTTGAGAGTTTTAAATTTAGATTAACACACAAAA 2028
Db 15878 ATATATTTTATATATATTTTATATTTTATATATATTTTATATATTTTGTCTCACAAATGATA 15933

RESULT 12

US-09-949-016-12423
; Sequence 12423, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12423
; LENGTH: 60376
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(60376)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12423

Query Match 3.4%; Score 68.8; DB 4; Length 60376;
Best Local Similarity 47.0%; Pred. No. 0.00018;
Matches 280; Conservative 0; Mismatches 312; Indels 4; Gaps 2;
Qy 1436 TATATGTGACAGATGTAAGTAATATATACATAAAATCATGTTTGTCTCAAGCATC 1495
Db 47378 TATTTATATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATA 47437
Qy 1496 TACGTTGAAATATATATAAGAGTTTTTTTTTGGTGAAAAAATATGATGAGAGTTTCAT 1555
Db 47438 TATATTTTATATTTTATATATATTTTATATATTTTATTTTATTTATATATATTTTATATA 47497
Qy 1556 CTTTCATAATAGTGAACAACTCTCTTCATACACCAAAAAAATTTGAAAAAATTAG 1615
Db 47498 TATTTTATATATTTTATATATATTTTATATATATTTTATATATATTTTATATATTTTA 47557
Qy 1616 TCAAACTCTCTTGTCCGATTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCAT 1675
Db 47558 TATATATTTTATATGATAT-ATTTTATATATTTTATATATTTTATATACATATTTTCATAT 47616
Qy 1676 AACAAATTTTTGGCATGGCAATTTATGTCGCGGTAAAAATATACCAATAGAAACATAT 1735
Db 47617 ATATTTTATATATTTTATATACATATTCATATATATTTTTTATATATTTTATATATACATAT 47676

Qy	1736	TTTTAGGAGTAGTAAAGATTATGATTGGAAGAAATACTATTACGATAAGCATARAATTTTC	1795
Db	47677	TTATATATACATATTTATATATATATACATATTTATATATATACACATATTTATATATAC	47736
Qy	1796	TTTTGCTGTTCTTGGTTTTTGGTTTTATAGAACATTGGAATATGTACTTTTGGTTTTTTT	1855
Db	47737	ATATATTTATTTATATATATATTTATTTATATATTTATATATTTATATATATATATAT	47796
Qy	1856	TCACCAGTAGATATGT--ACTATACACACATATAGTAACTGGGTAGTTTATATAGAGAG	1912
Db	47797	TTATATTTATATATATTTATATATTTATATATTTATATTTATATATTTATATATATTT	47856
Qy	1913	AGATTTGGATTTTTTCGTATATTTCTTTGTTGAAATAAATATGTCGTAATAATTTATGTTT	1972
Db	47857	ATATATTTATTTATATATTTTACATATATTTATATATTTATTTATTTATATTTATATTT	47916
Qy	1973	ATTAATTTGCAGATTTGTCACGTTTGAAGGTTTAATTTAGATTTAAACAACAAA	2028
Db	47917	ATATATTTTATATATATTTTATTTATTTATATATATTTGATTTTCTCTACCAATGATA	47972

RESULT 13

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US-09-949-016-15348
? Sequence 15348, Application US/09949016
? Patent No. 6812339
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSEQ for Windows Version 4.0
? SEQ ID NO 15348
? LENGTH: 134987
? TYPE: DNA
? ORGANISM: Human
US-09-949-016-15348

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[illegible]

RESULT 14

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US-09-949-016-15349
; Sequence 15349, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15349
; LENGTH: 134987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15349

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QY 1678 CAAATTTTGGCATGGCAATTAATGCTGCGAGTAAATATACCAATAGAAACATATTT 1737
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QY 1738 TTAGGAGTAGTAAAGATTATGATTGAAGAATACTATTACGATAAGCATAAATTTTCTT 1797
Db 11634 TTATATATATTTAT 11693
QY 1798 TTGCTGTTCTTGGTGGTTTGTGCTTTTATAGAACATTCGAATGATGACTTTTCTGTTTTTTC 1857
Db 11694 TAT 11753
QY 1858 ACCAGTAGATATGACTATACACATACATGAGTGGTAGTTTATATAGAGAGAGATT 1917
Db 11754 TAT 11813
QY 1918 TGATTTTTCGTATATTTCTTTTGTGGAATAAATATGCTGTAATAATTTTATTTATTA 1977
Db 11814 TAAATGTAATAAT 11873
QY 1978 TTTGACAGATTGTTTCACGTTGAGAGTTTAAATTTAGAT 2016
Db 11874 TAT 11912

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Job time : 350 secs

Db 11574 TATATATTTAT 11633
QY 1738 TTAGGAGTAGTAAAGATTATGATTGAAGAATACTATTACGATAAGCATAAATTTTCTT 1797
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Db 11874 TAT 11912

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; Sequence 15350, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15350
; LENGTH: 134987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15350

Query Match 3.3%; Score 67.8; DB 4; Length 134987;
Best Local Similarity 46.2%; Pred. No. 0.00035;
Matches 295; Conservative 0; Mismatches 342; Indels 2; Gaps 2;
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QY 1440 TTGATGCGAGATGAGAGTAATATATA-CATAAATCATGTTTGTCTCAAGCATCTAC 1498
Db 11334 TATTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11393
QY 1499 GTTGAATATATATAAGAGTTTGTGTTGGTGAATAAATATGATGAGAGTTCATCTT 1558
Db 11394 TAT 11453
QY 1559 TCATATAGTGAACAACTCTCTTTTCATACCAAAAAAAATTCGAAAAAAATAGTGA 1618
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QY 1619 AACTCTCTTTGTCGAGTTAGGT-TTGAGCTCAGAAATCAAAATACGATTAGCATAA 1677
Db 11514 TAT 11573

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignment)

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Title: US-10-643-676-1

Perfect score: 2030

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Scoring table: IDENTITY_NUC

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Searched: 9772231 seqs, 4124568258 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
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- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
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- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1064	52.4	1064	11	US-09-938-842A-4152
5	90.2	4.4	8056	20	US-10-473-126-386
6	88.4	4.4	115218	21	US-10-278-698-255
7	88.4	4.4	115218	21	US-10-278-698-769

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	9	79	3.9	8056	20	US-10-473-126-386	Sequence 386, App
c	10	78.8	3.9	15548	15	US-10-311-455-2128	Sequence 2128, App
	11	77.6	3.8	3673778	16	US-10-312-841-1	Sequence 1, Appli
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c	13	76	3.7	9810	15	US-10-311-455-399	Sequence 399, App
c	14	75.4	3.7	8961	15	US-10-240-453-302	Sequence 302, App
c	15	75	3.7	176096	22	US-10-981-277-34	Sequence 34, Appli
c	16	74.2	3.7	5413	18	US-10-221-714A-418	Sequence 418, App
c	17	73.2	3.6	6242	15	US-10-311-455-2121	Sequence 2121, App
c	18	72.4	3.6	19634	20	US-10-473-126-155	Sequence 155, App
c	19	72.4	3.6	19634	20	US-10-473-126-301	Sequence 301, App
c	20	72.2	3.6	478	19	US-10-021-323-6774	Sequence 6774, App
c	21	71.8	3.5	8056	20	US-10-473-126-240	Sequence 240, App
c	22	71.8	3.5	640681	9	US-09-790-988-1	Sequence 1, Appli
c	23	71.4	3.5	960	14	US-10-198-846-6381	Sequence 6381, A
c	24	71	3.5	529	19	US-10-021-323-10810	Sequence 10810, A
c	25	71	3.5	1501	20	US-10-473-126-328	Sequence 328, App
c	26	70.8	3.5	5979	14	US-10-239-676-18	Sequence 18, Appli
c	27	70.8	3.5	5979	15	US-10-240-453-26	Sequence 26, Appli
c	28	70	3.4	3673778	16	US-10-312-841-2	Sequence 2, Appli
c	29	69.4	3.4	11964	19	US-10-433-793-55	Sequence 55, Appli
c	30	69.4	3.4	158001	17	US-10-211-179-11	GENERAL INFORMATI
c	31	68.8	3.4	7498	15	US-10-311-455-230	Sequence 230, App
c	32	68.8	3.4	19787	15	US-10-311-455-1424	Sequence 1424, Ap
c	33	68.2	3.4	14023	15	US-10-311-455-2078	Sequence 2078, Ap
c	34	68.2	3.4	3673778	16	US-10-312-841-2	Sequence 2, Appli
c	35	67.8	3.3	6071	15	US-10-311-455-298	Sequence 298, App
c	36	67.8	3.3	6071	17	US-10-221-613-32	Sequence 32, Appli
c	37	67.6	3.3	8201	15	US-10-311-455-279	Sequence 279, App
c	38	67.6	3.3	8201	16	US-10-240-452-27	Sequence 27, Appli
c	39	67.4	3.3	8310	21	US-10-861-875-9	Sequence 9, Appli
c	40	67.2	3.3	6282	15	US-10-311-455-428	Sequence 428, App
c	41	66.8	3.3	6131	15	US-10-311-455-864	Sequence 864, App
c	42	66.6	3.3	1062	20	US-10-425-115-120013	Sequence 120013,
c	43	66.4	3.3	1179	20	US-10-363-345A-36195	Sequence 36195, A
c	44	66.4	3.3	1179	20	US-10-363-345A-36196	Sequence 36196, A
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ALIGNMENTS

RESULT 1

US-10-643-676-1
; Sequence 1, Application US/10643676
; Publication No. US20050176946A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry
; APPLICANT: Nuccio, Michael
; APPLICANT: Hsieh, Tzung-Fu
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis
; FILE REFERENCE: A35897-PCT-USA-A (072667.0188)
; CURRENT APPLICATION NUMBER: US/10/643,676
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: PCT/EP02/02894
; PRIOR FILING DATE: February 14, 2002
; PRIOR APPLICATION NUMBER: 60/270,779
; PRIOR FILING DATE: February 22, 2001
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2030
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-643-676-1

Query Match 100.0%; Score 2030; DB 22; Length 2030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTTCTAGAAGATCGACATTGAAGATACCTTCTCTTTCTATTTTATTGATTAG 60
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Db 61 AAAATCATATTCATTACAAAGGAAAAAATAAATTTTGTGATCCTAAAGTTATAAC 120
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Db 121 TTACAATTTTCCACACATTCAGTTGGTGGTAGTATTAATTTATCTATTTTATCAAAAGTTGG 180
Qy 181 TTTTAGGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAACTGAATT 240
Db 181 TTTTAGGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAACTGAATT 240
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Qy 301 GAAAAATAGAAATCGAATCAGCTTTGAGTGTAGAGGGATTGATATTTGGTCGACATTT 360
Db 301 GAAAAATAGAAATCGAATCAGCTTTGAGTGTAGAGGGATTGATATTTGGTCGACATTT 360
Qy 361 TAAAGAGTTGTTTGTGTTTTTTTCCAAATCTGCATGGTTTTTCGTTCCGTTGAACCAAAAT 420
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Qy 421 TCAACACTTTGTATATAACCGGAATAGTATAATACCTAGACGTACGCCAATACCAAAAAATAA 480
Db 421 TCAACACTTTGTATATAACCGGAATAGTATAATACCTAGACGTACGCCAATACCAAAAAATAA 480
Qy 481 ATTAATACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATCAGCAACTTA 540
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Db 601 CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTATAATACATTTGTTGTTA 660
Qy 661 AACAGATAATATACATTAATAGTATGAAATATGAATATAGATAAGAGGCGTA 720
Db 661 AACAGATAATATACATTAATAGTATGAAATATGAATATAGATAAGAGGCGTA 720
Qy 721 TATGTTACAACTACAGATCACCATCCCAATTAACAATCCGATTTGGTGGGCCCATTTGTT 780
Db 721 TATGTTACAACTACAGATCACCATCCCAATTAACAATCCGATTTGGTGGGCCCATTTGTT 780
Qy 781 TCGATATTTGCCAATCTGTGATGTAGCTGCGCAGCTGGCATATTTTCCCTCTGATT 840
Db 781 TCGATATTTGCCAATCTGTGATGTAGCTGCGCAGCTGGCATATTTTCCCTCTGATT 840
Qy 841 ACGTTTTTACCCCTTCTCTCTGTTTCCACGGTTAAATTTCAATTTTATTTTGTACCGCT 900
Db 841 ACGTTTTTACCCCTTCTCTCTGTTTCCACGGTTAAATTTCAATTTTATTTTGTACCGCT 900
Qy 901 GTCTTTTACCCCTTTTAAAGAAACCCCAACCCGAAATCATACTATACCGAAATCACATGT 960
Db 901 GTCTTTTACCCCTTTTAAAGAAACCCCAACCCGAAATCATACTATACCGAAATCACATGT 960
Qy 961 CTTTCATGGTGACGTAACAGACTTATTTTCCGGTTGAATTTGGTTTAACTTATTTGAGATT 1020
Db 961 CTTTCATGGTGACGTAACAGACTTATTTTCCGGTTGAATTTGGTTTAACTTATTTGAGATT 1020
Qy 1021 GTGCTAACCGGAAACAGAAACGGTTATGACGCCAACCGAGGCAAGGGGTTAAACGAGAA 1080
Db 1021 GTGCTAACCGGAAACAGAAACGGTTATGACGCCAACCGAGGCAAGGGGTTAAACGAGAA 1080
Qy 1081 AGAGGGATGCGAGAAATCGTAAATTAACAAGAAAAATAAAGGGTGGTTTTCACGATAAGTC 1140
Db 1081 AGAGGGATGCGAGAAATCGTAAATTAACAAGAAAAATAAAGGGTGGTTTTCACGATAAGTC 1140

Qy 1141 TGTCTATATGACCGGAAAGGGTTTTCTTAATTCAGAGAGACAATTAATCAGTTTCGTGTG 1200
Db 1141 TGTCTATATGACCGGAAAGGGTTTTCTTAATTCAGAGAGACAATTAATCAGTTTCGTGTG 1200
Qy 1201 TTTTGGAGAAAGAAAGAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTT 1260
Db 1201 TTTTGGAGAAAGAAAGAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTT 1260
Qy 1261 TCAAGTAAGTCTCTTTTATCAAACTCTTAATATAAAACAAATCAAAACATGAACACGTCGT 1320
Db 1261 TCAAGTAAGTCTCTTTTATCAAACTCTTAATATAAAACAAATCAAAACATGAACACGTCGT 1320
Qy 1321 TCTTCGTTTCGATCTAGATACGATTTTTCGAGATTAACAGAGGAAACAAAGTTAGTGATTAT 1380
Db 1321 TCTTCGTTTCGATCTAGATACGATTTTTCGAGATTAACAGAGGAAACAAAGTTAGTGATTAT 1380
Qy 1381 TACTAGGTTGTTTCAATATATTTTCCGAGATTAACAGAGGAAACAAAGTTAGTGATTAT 1440
Db 1381 TACTAGGTTGTTTCAATATATTTTCCGAGATTAACAGAGGAAACAAAGTTAGTGATTAT 1440
Qy 1441 TGATGCAGAGTATGAAGTAATATATACATAAAATCATGTTTTTGTCTCAAGCATCTACGT 1500
Db 1441 TGATGCAGAGTATGAAGTAATATATACATAAAATCATGTTTTTGTCTCAAGCATCTACGT 1500
Qy 1501 TGAATATATATAAGAAAGTTTTTTTTTGGTGAAGAAATATGTATGAGAAAGTTTCATCTTC 1560
Db 1501 TGAATATATATAAGAAAGTTTTTTTTTGGTGAAGAAATATGTATGAGAAAGTTTCATCTTC 1560
Qy 1561 ATAATAGTGAACCAACTCTCTTTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAA 1620
Db 1561 ATAATAGTGAACCAACTCTCTTTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAA 1620
Qy 1621 CTCTCTTTGTCGATAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATACAA 1680
Db 1621 CTCTCTTTGTCGATAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATACAA 1680
Qy 1681 ATTTTGGCATGGCAATTTATCTGTCAGGTAATAATATACCAATAGAAACATATTTT 1740
Db 1681 ATTTTGGCATGGCAATTTATCTGTCAGGTAATAATATACCAATAGAAACATATTTT 1740
Qy 1741 GGAGTAGTAAAGTATGATTGAAGAAATACTATTACGATAAGCATAAAAATTTCTTTT 1800
Db 1741 GGAGTAGTAAAGTATGATTGAAGAAATACTATTACGATAAGCATAAAAATTTCTTTT 1800
Qy 1801 CTGTTCTGGTTTTGTCGTTTTATAGAACATTTGAATATGTAATCTTTTGTGTTTTTTCACC 1860
Db 1801 CTGTTCTGGTTTTGTCGTTTTATAGAACATTTGAATATGTAATCTTTTGTGTTTTTTCACC 1860
Qy 1861 AGTAGATATGATACATACACATTAAGTACATGGGTAGTTTATATAGAGAGATTGA 1920
Db 1861 AGTAGATATGATACATACACATTAAGTACATGGGTAGTTTATATAGAGAGATTGA 1920
Qy 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAAATATGTGTAATAATTTATTTGTTTAAATTT 1980
Db 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAAATATGTGTAATAATTTATTTGTTTAAATTT 1980
Qy 1981 GACAGATTTGTTTCAAGTTGAGAGTTTAAATTTAGATTTAAACCAACAAAG 2030
Db 1981 GACAGATTTGTTTCAAGTTGAGAGTTTAAATTTAGATTTAAACCAACAAAG 2030

RESULT 2
US-10-643-676-2
; Sequence 2, Application US/10643676
; Publication No. US20050176946A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry
; APPLICANT: Nuccio, Michael
; APPLICANT: Heleh, Tzung-Fu
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis
; FILE REFERENCE: A35897-PCT-USA-A (072697.0188)
; CURRENT APPLICATION NUMBER: US/10/643,676


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Db 1927 TTTTTCGTAATATCTTTTGTGAAATAAATAATGTAATGTAATTTATGTTTATTAATTT 1986

Qy 1981 GACAGATTTGTTCAAGTTGGAAGTTTAAATTTAGATTAAACAAACAAAAG 2030
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Db 1987 GACAGATTTGTTCAAGTTGGAAGTTTAAATTTAGATTAAACAAACAAAAG 2036
|||||

RESULT 3
US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152

Query Match 52.4%; Score 1064; DB 9; Length 1064;
Best Local Similarity 100.0%; Pred. No. 4.6e-184;
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 GGTGACGTAAACAAGACTTATTTCCGGTTGAAATTTGGTTTAACTATGAGATTGTGCTA 1026
Db 1 GGTGACGTAAACAAGACTTATTTCCGGTTGAAATTTGGTTTAACTATGAGATTGTGCTA 60

Qy 1027 ACCGAAACAGAAACGGTTATGACGCCAACGAGCGGTTAAACGAGAAAGAGGG 1086
Db 61 ACCGAAACAGAAACGGTTATGACGCCAACGAGCGGTTAAACGAGAAAGAGGG 120

Qy 1087 GATGCGAGAAATCGTAATTAACAGGAAATAAAGGGTGGTTTCCACGATAAGTCTGCTA 1146
Db 121 GATGCGAGAAATCGTAATTAACAGGAAATAAAGGGTGGTTTCCACGATAAGTCTGCTA 180

Qy 1147 TATGACGCGAAAGGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTTGTTGGA 1206
Db 181 TATGACGCGAAAGGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTTGTTGGA 240

Qy 1207 GAACAAGAGACAGATCAATATAGCAGGAGATCTCTTAAGAGATTTATCGTTTCAAGT 1266
Db 241 GAAGAAGAAGAACAGATCAATATAGCAGGAGATCTCTTAAGAGATTTATCGTTTCAAGT 300

Qy 1267 AAGTCTCTTTTCAAACTCTTAATATAACAAATCAAAACATGAACACGTCGTCTCTTCG 1326
Db 301 AAGTCTCTTTTCAAACTCTTAATATAACAAATCAAAACATGAACACGTCGTCTCTTCG 360

Qy 1327 TTTTCGATTTAGATACGATTTTTCGAGATTTTTCGAGTGAATCTGTTTATTAATCTAG 1386
Db 361 TTTTCGATTTAGATACGATTTTTCGAGATTTTTCGAGTGAATCTGTTTATTAATCTAG 420

Qy 1387 GGTGTTTCATATTTTCCGAGATTTACCAGAGGACAAAGTTAGTGTATATTTATGATGC 1446
Db 421 GGTGTTTCATATTTTCCGAGATTTACCAGAGGACAAAGTTAGTGTATATTTATGATGC 480

Qy 1447 AGAGTGAAGTAATATATATACATAAAATCATGTTTGTCTTCAAGCATCTACGTTGAAAT 1506
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Db 481 AGAGTGAAGTAATATATATACATAAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 540

Qy 1507 ATATATAAGAAGTTTTTTTTTGTGAAAAAATATGTAATGAGAAGTTTCATCTTTCATAATA 1566
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Db 541 ATATATAAGAAGTTTTTTTTTGTGAAAAAATATGTAATGAGAAGTTTCATCTTTCATAATA 600
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Qy 1567 GTCAAAACAACCTCTCTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAAAACTCTCT 1626
Db 601 GTCAAAACAACCTCTCTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAAAACTCTCT 660
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Qy 1627 TTTGCCGATTTAGGTTTGGACTCAGAAATCAAAATACGATTAGCATAACAAAATTTT 1686
Db 661 TTTGCCGATTTAGGTTTGGACTCAGAAATCAAAATACGATTAGCATAACAAAATTTT 720
|||||
Qy 1687 TGGCATGGCAATTAATTTGCTGCGAGGTAATAATATACCAATAGAAAAACATATTTTAGAGTA 1746
Db 721 TGGCATGGCAATTAATTTGCTGCGAGGTAATAATATACCAATAGAAAAACATATTTTAGAGTA 780
|||||
Qy 1747 GTTAAAGATTATGATTGAAGAAATACATTACGATAAGCATAAAAAATTTCTTTTGCCTGTC 1806
Db 781 GTTAAAGATTATGATTGAAGAAATACATTACGATAAGCATAAAAAATTTCTTTTGCCTGTC 840
|||||
Qy 1807 TTGGTTTTTTCGTTTATAGAAACATTGAATATGTAATTTTGTGTTTTCACACAGTAGA 1866
Db 841 TTGGTTTTTTCGTTTATAGAAACATTGAATATGTAATTTTGTGTTTTCACACAGTAGA 900
|||||
Qy 1867 TATGTACTATACACATACATTAAGTAACATGGTAGTTTATATAGAGAGATTTGATTTTTC 1926
Db 901 TATGTACTATACACATACATTAAGTAACATGGTAGTTTATATAGAGAGATTTGATTTTTC 960
|||||
Qy 1927 GTATATTTCTTTTGTGAAAAATAATATGTAATAATTTATGTTTATTAATTTTGACAGA 1986
Db 961 GTATATTTCTTTTGTGAAAAATAATATGTAATAATTTATGTTTATTAATTTTGACAGA 1020
|||||
Qy 1987 TTTGTTCCAGTTGAGAAGTTTAAATTTAGATTAAACAAACAAAAG 2030
Db 1021 TTTGTTCCAGTTGAGAAGTTTAAATTTAGATTAAACAAACAAAAG 1064
|||||

RESULT 4
US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152

Query Match 52.4%; Score 1064; DB 11; Length 1064;
Best Local Similarity 100.0%; Pred. No. 4.6e-184;
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 GGTGACGTAAACAAGACTTATTTCCGGTTGAAATTTGGTTTAACTATGAGATTGTGCTA 1026
Db 1 GGTGACGTAAACAAGACTTATTTCCGGTTGAAATTTGGTTTAACTATGAGATTGTGCTA 60
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1027 ACCGAAACAGAAACGGTTATGCGCCAAACGAGCGGCTAAACAGGAAGAGGG 1086
Db ACCGAAACAGAAACGGTTATGCGCCAAACGAGCGGCTAAACAGGAAGAGGG 120
1087 GATGCGAGAAATCGTAATTAACAGGAAATAAAGGGTGGTTTCACGATAGTCTGCTA 1146
Db GATGCGAGAAATCGTAATTAACAGGAAATAAAGGGTGGTTTCACGATAGTCTGCTA 180
1147 TATGACGCGAAAGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTTGGTGG 1206
Db TATGACGCGAAAGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTTGGTGG 240
1207 CAAGAGAGAGACAGATCAATATACGAGAGAGATCTCTAAGAGAGATTTATCGTTTCAAGT 1266
Db CAAGAGAGAGACAGATCAATATACGAGAGAGATCTCTAAGAGAGATTTATCGTTTCAAGT 300
1267 AAGTCTCTTTATCAAACTCTTAAATATAAACAACAAATCAAAACATGACGTCGTCTTCG 1326
Db AAGTCTCTTTATCAAACTCTTAAATATAAACAACAAATCAAAACATGACGTCGTCTTCG 360
1327 TTTGCAATCTAGATACGATTTTTAGTTTCATGTGAATGAACTCTGTTTTTACTACTAG 1386
Db TTTGCAATCTAGATACGATTTTTAGTTTCATGTGAATGAACTCTGTTTTTACTACTAG 420
1387 GGTGTTCAATATTTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGATTAATTTGATGC 1446
Db GGTGTTCAATATTTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGATTAATTTGATGC 480
1447 AGAGTATCAAGTAATATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 1506
Db AGAGTATCAAGTAATATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 540
1507 ATATATAAGAAAGTTTTTTTTTGGTGAAAAAAATATGATATGAGAAGTTCACTTTCAATA 1566
Db ATATATAAGAAAGTTTTTTTTTGGTGAAAAAAATATGATATGAGAAGTTCACTTTCAATA 600
1567 GTGAAACAACCTCTCTTATACACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCT 1626
Db GTGAAACAACCTCTCTTATACACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCT 660
1627 TTGTCGCAATAGTTAGTTGGTCTCAGAACTCAAAATACAGATTAGCATAAACAAATTTTT 1686
Db TTGTCGCAATAGTTAGTTGGTCTCAGAACTCAAAATACAGATTAGCATAAACAAATTTTT 720
1687 TGGCATGGCAATTAATGTCGAGGTAAATAATACCAATAGAAACATATTTTGGAGGTA 1746
Db TGGCATGGCAATTAATGTCGAGGTAAATAATACCAATAGAAACATATTTTGGAGGTA 780
1747 GTTAAGATTAATGTTGAAGAAATACATTTACGATTAAGCAATAAATTTCTTTGCTGTC 1806
Db GTTAAGATTAATGTTGAAGAAATACATTTACGATTAAGCAATAAATTTCTTTGCTGTC 840
1807 TTGGTTTTGTCGTTTTATAGAACTTGAATATGTAATTTGTTTTTTTACCAGTAGA 1866
Db TTGGTTTTGTCGTTTTATAGAACTTGAATATGTAATTTGTTTTTTTACCAGTAGA 900
1867 TATGTACTATACACATAGTAACATGGGTAGTTTATATAGAGAGAGATTTGATTTTTC 1926
Db TATGTACTATACACATAGTAACATGGGTAGTTTATATAGAGAGAGATTTGATTTTTC 960
1927 GTATATTTCTTTGTTGAAAAATAAATATGCTGTAATAATTTATTTGTTTAAATTTGCAGA 1986
Db GTATATTTCTTTGTTGAAAAATAAATATGCTGTAATAATTTATTTGTTTAAATTTGCAGA 1020
1987 TTTGTTACGTTGAGAGTTTAAATTTAGATTAAACAAACAAAAAG 2030
Db TTTGTTACGTTGAGAGTTTAAATTTAGATTAAACAAACAAAAAG 1064

RESULT 5

US-10-473-126-386/c

; Sequence 386, Application US/10473126

; Publication No. US20040234973A1

; GENERAL INFORMATION:

; APPLICANT: Epigenomics AG

; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: Proliferative disorders

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/473.126

; CURRENT FILING DATE: 2003-09-26

; NUMBER OF SEQ ID NOS: 1258

; SEQ ID NO 386

; LENGTH: 8056

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-473-126-386

Query Match 4.4%; Score 90.2; DB 20; Length 8056;

Best Local Similarity 42.2%; Pred. No. 4e-06;

Matches 840; Conservative 0; Mismatches 1128; Indels 23; Gaps 5;

Qy	27	AATACCTTCTCTTCTCTTCTATTTTATTTGATTTAGAAAATCATATTTCAATACAAAAGGAAA	86
Db	1993	AATAAAAAATTAATATTAATATTTTATTTTAAAAAATTAATTTTTTATTATTTATATA	1934
Qy	87	AAAAAAATAATTTTTTGTATCTCTAAAGTTATAACTTACAATTTTCCACACTTCAGTTGG	146
Db	1933	ATTTAATTTATTTTTTTTATTAATAATTTTATTTTATAATAAAAAATAAAAAATAAT	1874
Qy	147	TAGTATTAAATTTATCTATTTTATCAAAAGTTGGTTTGTAGGAAAAATGATCTTTTCATA	206
Db	1873	TAATTAATAATTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAACAAAAATTTATTTATTA	1814
Qy	207	TAAAAATATATAGATCTTCAAGAAACTGAATTTGGGTTTTTCAACTATTTTATCGTTGA	266
Db	1813	TTAAATTTAAATATAATAAATAATTAATTTTAAATTTTAAATTTTAAATAATTTTATA	1754
Qy	267	CACACTTTTGACTTATCAAAAAGAGTTCAAAATAGAAAAATAGAAATCGAATCACAAGTT	326
Db	1753	TTTTAATTTTTTAAATAATTAATAATTAATAATATAATTAATTAATAATAATTTTATA	1694
Qy	327	CAGTGAAGAGGGATTGATATGTGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCC	386
Db	1693	TAAATTTAAATAAAAAATTTTATCATATTAATTAATAATAATTTTAAATTTTAAATTTA	1634
Qy	387	AATCTGCAATGTTTTCGTTGGAACCAAACTCAACACTTTTGTATATAACCGAATAGT	446
Db	1633	ATTCATTTTATTTCAATTTTTTAAATAATTAATAATTAATAATAATAATTTTAAATTTA	1577
Qy	447	AATATACTAGACGTACGCAATACCAAAAAATAAAAAATTAATACTCAATTCACAAATTTGA	506
Db	1576	AATTTAATAATAATTTTTTAAAAAATAATTTTATTTTAAAAAATTTTAAACATATTTAT	1517
Qy	507	CTACACCATATCATGCATATATATCAGCAACCTAGATAATCAATGAATTTAATCGAGG	566
Db	1516	ATTTTATATTTATATAATAATTAATTTAATAATTAATTTTAAATAATAATAATTTTATA	1457
Qy	567	ATAATCAATATCCAATCAACGATATCAAGAGCCCTAATAATAGATCAATGAATCAAAAT	626
Db	1456	AAATAATTTTATTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAATAAAAAAATAAAAAAT	1397
Qy	627	AACATAACATAGTAATATACATTTGATTTGTGTAAACAGAAATAATATACATATATAGT	686
Db	1396	TTATTTTATATAAAAAAATAAATTTTAAATAAAAAATAAATAATTTAAATTTATTTTAA	1337
Qy	687	ATGAAAAATATGAATATAATAGATAGAGCGGCTATATGTTTCAACTACAGATCACCATCC	746
Db	1336	TTAAAAATTTATAATAAATTTTTTTTTTATTAATTTTAAATTTTAAAAAATAATTTACA	1277
Qy	747	ACAAATTAACAATCCGATTTGGTGGGCCCATTTGTTTCGATATTTTGCACACTGATTGATG	806
Db	1276	TATATTAATAATAATTAACATAACATTTTTTTTTTTTATTTCAAAAAAATAATTTATTA	1217

Qy	807	TGACTGCCAGCTGGCAGATATTTTCCCTCGCTCGATTACGTTCAGTTTTTAACCTTTCTCTCTGTT	866
Db	1216	AAATTTAAATTTAAATAAATTTAAAAATTTTAAAATAAATTTAAATA-----TAATCAAAA	1165
Qy	867	TCACGGTTAAATTCGAATTTTACTATTTTGTCACGCTGTCTTTACACCTTTTAAAGAAACCCC	926
Db	1164	ATATATTAAATTTTAAATTTTCAAATATCAAAAAAAATATTAAAAACAATAATATATAACAT	1105
Qy	927	AACCCGAAATCATAACTATATACCGAAATCACATGTCTTCATGGTCGACGTAAACAAGACTTAT	986
Db	1104	TTTAAACATTTAAAAAAAACAAATTAACAACAAATTTTATTATTACATATTAAAT	1045
Qy	987	TTTCCGGTTGAATTTGGTTTAAACCTATTGAGATTGTGCTAACCGAAACAGAAACGGTTA	1046
Db	1044	TTCAAAATTTAAAAAATAATAAAAAAATTTTAAAAATAATTTATTTTAAAAAATAATAAT	985
Qy	1047	TGACGCCAACGAGCGAAGGGGTAAACGAGAAAGAGGGGATGCAGAAATCGTAATTA	1106
Db	984	ATATATTATTATTCATTTAAATPAAAAAAATAAAAAATTTATTTTAAAAAAAATTTATTACA	925
Qy	1107	ACAAGGAAAAATAAAGGGTGGTTTCAACGATAAGTCTGCTATATGACGCGAAAGGGTTCT	1166
Db	924	AAAACAACAAATAATTTAAATATATAATTTAAATATATACAAATTTTATACATAAAA	865
Qy	1167	TAAATTCAGAGAGACAAATTAATCAGTTTCGTCGTTGGAGAGAAGAACAGACAGATCAA	1226
Db	864	AAAAATAAAAAAACAATTTTTTTTAAATAAAAAATTTTAAATAATCATTTATAAATTA	805
Qy	1227	ATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTHAGTCTCTTTATCAACTCT	1286
Db	804	TTTTTAAATATATAATAATAATAATTTTATAAATTTTAAATTTTAAATTTAAAAAAT	745
Qy	1287	TAATATAAACAAAAATCAAAACATGAACGCTGCTCTCGTTTCGATTCAGATACGATT	1346
Db	744	T-----TAAATATATAATAATAATTTTAAATTTAAATTTTAAATATAAAAAAATTT	694
Qy	1347	TTTTTAGTTTCATGTGAATGAACCTCTGTTTTATTACTACTAGGGTTGTTCAATATTTTTCCG	1406
Db	693	TTTTTATATTATTTTTTTTTTTTTTTTTAAATAAAATTTATATTTAAAAAATTTATTTAA	634
Qy	1407	AGAATTCACGAGAGAACAAAGTTAGTGATATATNTGATGCAGAGATATGAAGTAATTATAT	1466
Db	633	AAAAATTTTAAATTTTATATAATATTTTTTTTATAAATATTAATTATTAATAATAAATTT	574
Qy	1467	ACATAAATCATGTTTGTCTCAAGACCTACGTTGAAATATATATAAGAAAGTTTTTTTTT	1526
Db	573	TAATAAACAATTTAATAATATATA-AAATTTTAAATTTTAAATATATAATATTTAAATAT	515
Qy	1527	TGGTGAIAAAAAATATGTATGAGAAGTTCATCTTTCATAATAGTGAACAACCTCTCTTTCAT	1586
Db	514	TATAAATATTATAAATTTTAATTTTTTTTATTTAAATATATTTTATTTTAAAAATTAAT	455
Qy	1587	ACCAAAAAAAAAATTTGAAAAAAAAATTAGTGAAACTCTCTTTGTCGAGTTAGGTTAGGTT	1646
Db	454	TTTTTTTTTATTATTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT	395
Qy	1647	TGGACTCAGATCAAAATACGATTAGCATACAAATTTTTTTGGCATGCGCAATTAATTCGT	1706
Db	394	TTAAATATAAATAATTTTATTTCATTTTTTTTTTTTTTTTTTAAATATATTATTTTTATTTA	335
Qy	1707	GCAGGTAAAAATATACCATAGAAACATATTTTTTAGGAGTAGTTAAGATTTATGATTGAAGA	1766
Db	334	TTTTTTATTAAATTTTTTTTTTAAABAAATTTTTTAAAAAATAAATAAATTTTTTTTATTA	275
Qy	1767	AATACTATTACGATAAGCATAAAAATTTTCTTTTGTGCTGTTCTTGGTTTTGTGCGTTTTATA	1826
Db	274	AAATAAAATTT--TAAAAATTTTAAAAATTTTAAAAATTTTAAAAAATTTTAAAAATATTTT	217
Qy	1827	GAACATTTGAATATGCTCTTTTGTTTTTTTTCCACCAGTAGATATGCTACTATACACACATAA	1886
Db	216	AAAAATATAATAATTTTAAATTTTAAATTTTAAATAAATAAATAAATAAATAAATAAATAA	157
Qy	1987	GTAACATGGGTAGTTTATATATAGAGAGAGATTTGATTTTTTTCGTATATTTCTTTCTGTGAAA	1946

Query Match 3.7%; Score 75.4; DB 15; Length 8961;
Best Local Similarity 45.1%; Pred. No. 0.0021;
Matches 329; Conservative 0; Mismatches 391; Indels 9; Gaps 1;

QY 30 ACTTCTCTTTCTATTTTATTTGATTTAGAAATCATATTCATATCAAAAGGAAAAA 89
DB 5907 ACGAACTCCTTACAAATTTATATAAAATATCAAAATATATAAATAAATAAATATTTAT 5848
QY 90 AAAATAAATTTTGTCTTAAAGTTTAACTTCAAAATTTTCCACACTTCAGTTGGTAG 149
DB 5847 AAAATAAATTTTCCAAATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATA 5788
QY 150 TATTAATTTATCTATTTTATCAAAAGTTTGGTTTATAGGAAAAATGATCTTTTCATATA 209
DB 5787 AAACATTTAAATTTTAAATTTCTTTTAAATAAATAAATAAATAAATAAATAAATAA 5728
QY 210 AAAATATATAGATCTTCAAAAGAACTGAATTTGGTTTCAACTATTTTATCGTTTGAC 269
DB 5727 AAAACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5668
QY 270 TACTTTGACTTATCAAAAGAGTTCAAAATAGAAAAATAGATCGAATCACAGTTTCAG 329
DB 5667 TAAAAACAACCTTAAAAAATAAATTTATTAATAATATCAATATAAATAAATAAATAA 5608
QY 330 TGTAAGAGGGATTTGATATTTGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCCAA 389
DB 5607 TTATTCAGAAATATAT-----ATAAATAAATAAATAAATAAATAAATAAATAAATA 5557
QY 390 CTGCAATGTTTTCGTTCCGTTGAACCAAAATTCACACTTTTGTATATAAACCAGTAAT 449
DB 5556 AAAAAAATAAATTTCTAACTATTATAAATAATCAAACTAAAAATAAATAAATAAATA 5497
QY 450 ATACTAGAGTACGCAATACCAAAATAAATAAATAAATAAATAAATAAATAAATAAATA 509
DB 5496 ATTATAAATAATCTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 5437
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DB 5436 CGAAATAATCTATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 5377
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QY 750 ATTAACAAT 758
DB 5196 TATATATAT 5188

RESULT 15
US-10-981-277-34
; Sequence 34, Application US/10981277
; Publication No. US20050181389A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Compositions and Methods for Glioma Classification
; FILE REFERENCE: 03-968-US
; CURRENT APPLICATION NUMBER: US/10/981.277
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,817
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34

LENGTH: 176096
TYPE: DNA
ORGANISM: Homo sapiens
US-10-981-277-34

Query Match 3.7%; Score 75; DB 22; Length 176096;
Best Local Similarity 46.8%; Pred. No. 0.008;
Matches 301; Conservative 0; Mismatches 340; Indels 2; Gaps 2;

QY 46 TTTTATTTGATTTAGAAATCATATTCATTAACAAAGGAAAAAATAAATTTTGTGTA 105
DB 166681 TATTATATTAT 166740
QY 106 TCCTAAAGTTTAACTTACAAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTAT 165
DB 166741 ATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 166800
QY 166 TTTATCAAAAGTTTGGTTTATAGGAAAAATGATCTTTTCATATAAATAAATAAATA 225
DB 166801 ATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 166860
QY 226 CAAGAAACTGAATTTGGGTTTTCACACTATTTTATCGTTTGACACTTCTGACTTATCAA 285
DB 166861 ATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 166920
QY 286 AAAGAGTTTCAAAATAGAAAAATAGAAATCGAATCGAATCGTTTTCAGTGAAGGGATTTGA 345
DB 166921 ATTATATTAT 166980
QY 346 TATTGGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCCAACTCGCATGTTTTCGT 405
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QY 406 TCCGTTGAACCAAAATTCACACTTTGTATAAACCGAATAGTAATATCTAGACGTACGCC 465
DB 167041 TATATTAT 167100
QY 466 AATACCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 525
DB 167101 AAT 167160
QY 526 TATATCAGCAACCTTGAATAATCAATGAAATTTTAAATCGAGGATATCAATATCCAACTCA 585
DB 167161 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 167219
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DB 167220 TTAATAATTTTAT 167279
QY 646 CATTCATTTTGTGTTAAACAGAAATAAATAAATAAATAAATAAATAAATAAATAAATA 688
DB 167280 TATT-ATATGTTATATACATTAACATATATTTTATATATATATATATATATAT 167321

Search completed: October 24, 2005, 01:24:02
Job time : 1660 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 08:58:27 ; Search time 6674 Seconds

(without alignment)
11577.834 Million cell updates/sec

Title: US-10-643-676-1

Perfect score: 2030

Sequence: 1 cttcatgaaggatggacca.....ttagattacaacaaaaag 2030

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gse1.*

9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	669.4	33.0	679	8 AQ961292	AQ961292 LERFK31TF
C 2	663	32.7	679	8 AQ961293	AQ961293 LERFK31TR
C 3	426	21.0	426	9 CC796106	CC796106 SALK_0928
C 4	363.8	17.9	412	8 BZ597205	BZ597205 SALK_1004
C 5	311.8	15.4	396	9 CC796100	CC796100 SALK_0927
C 6	309.6	15.3	931	9 CL483650	CL483650 SAIL_384
C 7	256	12.6	223	8 BZ355348	BZ355348 SALK_1265
C 8	230	11.3	246	8 BH809771	BH809771 SALK_0056
C 9	156.6	7.7	749	8 BZ062372	BZ062372 l1e85b02.
C 10	147	7.2	713	8 BH439107	BH439107 BOHAK61TR
C 11	134.8	6.6	194	9 CR402809	CR402809 Arabidops
C 12	130	6.4	597	8 BH745927	BH745927 gz74a08.b
C 13	125.2	6.2	982	9 CL489509	CL489509 SAIL_525
C 14	119.6	5.9	786	8 BH425990	BH425990 BOGJF07TR
C 15	93.6	4.6	1592	9 CG750135	CG750135 P044-3-B0
C 16	93	4.6	207	1 AV832342	AV832342 Arabidops
C 17	93	4.6	1101	9 CNG0039G	AL063921 Drosophil
C 18	92.8	4.6	507	1 AV825689	AV825689 AV825689
C 19	92.4	4.6	278	1 AJ609323	AJ609323 AJ609323
C 20	90.4	4.5	605	5 BP562932	BP562932 BP562932
C 21	89.2	4.4	1101	9 CNG000EVL	AL069706 Drosophil
C 22	88.4	4.4	495	7 T43150	T43150 6413 Lambda
C 23	87.8	4.3	636	5 BP561393	BP561393 BP561393
C 24	87.6	4.3	1896	9 CG753083	CG753083 P048-1-CO

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C 26	87.2	4.3	1101	9 CNG000EVL	AL069706 Drosophil
C 27	87	4.3	516	7 H36351	H36351 14873 Lambda
C 28	86	4.2	1202	8 CC262481	CC262481 CH261-167
C 29	85.4	4.2	660	9 BH183498	BH183498 023.L.07-
C 30	85.4	4.2	660	9 CNG070NJ	AL620449 T3 end of
C 31	82.8	4.1	1190	9 CNG020N7	AL206908 Tetraodon
C 32	82.6	4.1	1101	9 CNG00KAE	AL077628 Drosophil
C 33	82.6	4.1	1225	9 CNG0161D	AL106171 Drosophil
C 34	82.4	4.1	515	7 CK119189	CK119189 213m19.p1
C 35	82.4	4.1	894	7 CF652281	CF652281 45-L02052
C 36	82.4	4.1	1101	9 CNG003BD	AL064091 Drosophil
C 37	81.8	4.0	1378	9 AG350209	AG350209 Mus muscu
C 38	81.4	4.0	2087	9 AG333887	AG333887 Mus muscu
C 39	81.2	4.0	1258	9 CL508886	CL508886 SAIL_804
C 40	81	4.0	1592	9 CG750135	CG750135 P044-3-D0
C 41	80.6	4.0	826	9 AG579614	AG579614 Mus muscu
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C 43	80.6	4.0	1391	9 CG754863	CG754863 P050-2-G0
C 44	80.4	4.0	722	7 CV481731	CV481731 AGENCOURT
C 45	80	3.9	782	7 CV484987	CV484987 AGENCOURT

ALIGNMENTS

RESULT 1
AQ961292/c
LOCUS LERFK31TF LERA Arabidopsis thaliana genomic clone LERFK31, genomic survey sequence. 679 bp DNA linear GSS 28-JAN-2000
ACCESSION AQ961292
VERSION AQ961292.1 GI:6788993
KEYWORDS GSS
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 679)
AUTHORS Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
TITLE Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
JOURNAL Unpublished (2000)
COMMENT Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atotigr.org
For additional information, see <http://www.tigr.org/tadb/at/at.html>
Seq primer: TF
Class: shotgun.

FEATURES

Location/Qualifiers
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/clone_lib="LERFK31"
/clone_lib="LERA"
/note="Organ: Leaf; Vector: PHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."

ORIGIN

Query Match 33.0%; Score 669.4; DB 8; Length 679;
Best Local Similarity 99.1%; Pred. No. 2.1e-105;
Matches 673; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1132 CGATAAGTGTGCTATATGACCGCAAGGGTTTCTTAATTGAGAGACAATTATCAG 1191
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Db 679 CGATAAGTCTGCTATATGACCGGAAGAGTTTCTTAAATTCAGAGACAAATTAATCAG 620
Qy 1192 TTTCTGTGTTTGGAGAGAGAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGA 1251
Db 619 TTTCTGTGTTTGGAGAGAGAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGA 560
Qy 1252 TTTATCGTTTCAAGTNAAGTCTCTTTATCAAACTCTTAATATATAACAAATCAAAACATGAA 1311
Db 559 TTTATCGTTTCAAGTNAAGTCTCTTTATCAAACTCTTAATATATAACAAATCAAAACATGAA 500
Qy 1312 CACGTGCTGCTCTCGTTTCGATCTTAGATACGATTTTATAGTTTCATGTGAATGAATCTG 1371
Db 499 CACGTGCTGCTCTCGTTTCGATCTTAGATACGATTTTATAGTTTCATGTGAATGAATCTG 440
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Qy 1492 CATCTACGTTGAAATATATATAAGAGTTTGTGTAAGAAATATGTATGAGAAGT 1551
Db 319 CATCTACGTTGAAATATATATAAGAGTTTGTGTAAGAAATATGTATGAGAAGT 260
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Db 139 ACATAACAAATTTTGGCTGCAATTAATGTCTGCAAGTAAATATACCAATAGAAAC 80
Qy 1732 ATATTTTAGGAGTGTAGTATGATTAAGTAAAGAAATATCTATTACGATAAGCAATAAT 1791
Db 79 ATATTTTAGGAGTGTAGTATGATTAAGTAAAGAAATATCTATTACGATAAGCAATAAT 20
Qy 1792 TTTCTTTTGTGCTCTGG 1810
Db 19 TTTCTTTTGTGCTCTGG 1

RESULT 2
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DEFINITION LERFK31TR LERA Arabidopsis thaliana genomic clone LERFK31, genomic survey sequence.
ACCESSION AQ961293
VERSION AQ961293.1 GI:6788994
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 679)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
JOURNAL Unpublished (2000)
COMMENT Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org

For additional information, see <http://www.tigr.org/cdb/at/at.html>
Seq primer: TR
Class: Shotgun.
Location/Qualifiers
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/mol_type="genomic DNA"
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/notes="Organ: Leaf; Vector: phos1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."
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Query Match 32.7%; Score 663; DB 8; Length 679;
Best Local Similarity 98.5%; Pred. No. 2.7e+104;
Matches 669; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 939 TAACTATACGAAATCACATGCTTTCATGTGAGCTAACAGACTTATTTCCGGTTGAA 998
Db 1 TAACTATACGAAATCACATGCTTTCATGTGAGCTAACAGACTTATTTCCGGTTGAA 60
Qy 999 TTTGGTTTAACTTATTCAGATTGTGCTAACCGAAAAACAGAAACGGTTATCGACGCAACGA 1058
Db 61 TTTGGTTTAACTTATTCAGATTGTGCTAACCGAAAAACAGAAACGGTTATCGACGCAACGA 120
Qy 1059 GCGAAGAGGGGTAAACAGAGAAAGAGGGGATGCGAGAAATCGTAATTAACAAGAAAAATA 1118
Db 121 GCGAAGAGGGGTAAACAGAGAAAGAGGGGATGCGAGAAATCGTAATTAACAAGAAAAATA 180
Qy 1119 AAGGTGTTTTCAGGATAAGTCTGTCTATATGACGGAAGGGTTTCTTAATTCAGAGA 1178
Db 181 AAGGTGTTTTCAGGATAAGTCTGTCTATATGACGGAAGGGTTTCTTAATTCAGAGA 240
Qy 1179 GACAAATTAATCAGTTTCGTGTTGGAGAAAGAGAAACAGATCAATACAGAGGAGAG 1238
Db 241 GACAAATTAATCAGTTTCGTGTTGGAGAAAGAGAAACAGATCAATACAGAGGAGAG 300
Qy 1239 ATCTCTAAAGAGATTATTCGTTTCAAGTAAAGTCTCTTTTATCAAACTCTTAAATAAACA 1298
Db 301 ATCTCTAAAGAGATTATTCGTTTCAAGTAAAGTCTCTTTATCAAACTCTTAAATAAACA 360
Qy 1299 ATCAAAACATGAACAGCTGCTGTTCCGATCTAGATACGATTTTATAGTTTCATG 1358
Db 361 ATCAAAACATGAACAGCTGCTGTTCCGATCTAGATACGATTTTATAGTTTCATG 420
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Qy 1419 GGAACAAAGTTAGTATTATATTTGATGACGAGATGAAGTAATATATATATATATATATAT 1478
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Db 601 ATGTATGAGAAGTTTCATCTTTTCAATATAGTGAACAACTCTCTTTTATATACCAAAAAAAA 660
Qy 1599 ATTTGAAAAAATTAAGTG 1617
Db 661 ATTTGAAAAAATTAAGTG 679
RESULT 3
LOCUS CC796106/c
DEFINITION CC796106 .55.75.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_092802.55.75.x, genomic

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survey sequence.
ACCESSION CC796106 GI:32391329
VERSION CC796106.1
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 426)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
          Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
          Shinn,P., Zimmerman,J. and Ecker,J.R.
          A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
          Unpublished (2001)
          Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: ecker@salk.edu
          This is single pass sequence recovered from the left border of
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              /note="PCR was performed on Arabidopsis thaliana lines
              each of which contains one or more TDNA insertion
              elements. The resultant fragment for each line was
              directly sequenced to determine the genomic sequence at
              the site of insertion. Details of the protocols used can
              be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES             source
    source
    Class: TDNA tagged.
    Location/Qualifiers
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        /mol_type="genomic DNA"
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        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
        /note="PCR was performed on Arabidopsis thaliana lines
        each of which contains one or more TDNA insertion
        elements. The resultant fragment for each line was
        directly sequenced to determine the genomic sequence at
        the site of insertion. Details of the protocols used can
        be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      21.0%; Score 426; DB 9; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 153 TAATTATCTATTTTATCAAAAGTTTGGTTTATAGGAAAATGATCTTTTCATATAAAAA 212
DB 426 TAATTATCTATTTTATCAAAAGTTTGGTTTATAGGAAAATGATCTTTTCATATAAAAA 367
QY 213 ATATATAGATCTTCAAGAAATGAAATGGGTTTCAACTATTTTATCGTTTGACACTAC 272
DB 366 ATATATAGATCTTCAAGAAATGAAATGGGTTTCAACTATTTTATCGTTTGACACTAC 307
QY 273 TTTGACTTATCAAAAGAGTTCAAATACAAAATAGAAATCGAATCACAACGTTTTCAGTCT 332
DB 306 TTTGACTTATCAAAAGAGTTCAAATACAAAATAGAAATCGAATCACAACGTTTTCAGTCT 247
QY 333 AAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCCAAATCG 392
DB 246 AAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCCAAATCG 187
QY 393 CATGTTTTTTCGTTTCGTTGAACCAAAATTCACACATTTGTTATTAACCGAATAGTATATA 452
DB 186 CATGTTTTTTCGTTTCGTTGAACCAAAATTCACACATTTGTTATTAACCGAATAGTATATA 127
QY 453 CTAGAGCTAGCCAAATACCAAAATATAAATTAACCTCAATTCACAAATTTGAATCTACAC 512
DB 126 CTAGAGCTAGCCAAATACCAAAATATAAATTAACCTCAATTCACAAATTTGAATCTACAC 67
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RESULT 4
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LOCUS BZ597205
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Arabidopsis thaliana genomic clone SALK_100410.46.60.n, genomic
survey sequence.
ACCESSION BZ597205
KEYWORDS BZ597205.1 GI:27538158
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 412)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
          Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
          Shinn,P., Zimmerman,J. and Ecker,J.R.
          A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
          Unpublished (2001)
          Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: ecker@salk.edu
          This is single pass sequence recovered from the left border of
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          Class: TDNA tagged.
          Location/Qualifiers
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              the site of insertion. Details of the protocols used can
              be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      17.9%; Score 363.8; DB 8; Length 412;
Best Local Similarity 94.2%; Pred. No. 9.9e-53;
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QY 1382 ACTAGGGTTGTTCAATATATTTTCCGAGATTTACCAGAGGACAAAGTTAGTGATTATATT 1441
DB 61 ACTAGGGTTGTTCAATATATTTTCCGAGATTTACCAGAGGACAAAGTTAGTGATTATATT 120
QY 1442 GATCAGAGTATGAAGTAATATATATACATAAATCATGTTTGTTCACAGCATCTACGTT 1501
DB 121 GATCAGAGTATGAAGTAATATATATACATAAATCATGTTTGTTCACAGCATCTACGTT 180
QY 1502 GAAATATATATAAGAGTTTTTTTTTGGTGAATAAATATGTATGAGAGTTTCATCTTTCA 1561
DB 181 GAAATATATATAAGAGTTTTTTTTTGGTGAATAAATATGTATGAGAGTTTCATCTTTCA 240
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QY 1181 CAATTAATCAGTTCGTGTTGTTGAGAGAAAGAACACAGATCAATACGAGGAGAT 1240
Db 197 CTCCACTCCTATCGGAGCTTGACTAAAGAAAGAACATATCGATGCAAGGTAAAT 256
QY 1241 CTCTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTTAATAAACAAT 1300
Db 257 CTGTAAAGAGATGATGCTCTATGCAAAATACCTTTTATCAAACTCTTAAAGAAACAAT 316
QY 1301 CAAAACATGAACAGTCTGTCGTTGCTGATCTAGATAGATTTTATGTTTCATG 1360
Db 317 AAAACATGAACAGCGGAGCATTTGGTGGCATATTTCAAAACAATTTTATATCATG 376
QY 1361 AATGAACCTGTTTATTAATCTAGTGGTGTGTCATATTTTCCGAGAAATTTACAGAG 1420
Db 377 AATGAACCTGTTTATTAATCTAGTGGTGTGTCATATTTTCCGAGAAATTTACAGAG 436
QY 1421 AACAAAGTTAGTGAATATATGATGACAGATGATGAAGTAATATATATACATAATCATG 1480
Db 437 ACA-----AGTTAAGCTTTATTTGGCGAGATACGAAAGAAATCTATCTTAAATCATGCC 491
QY 1481 TTGTTCTCAAGCATCTAGTGAATATATATGAAAGTCTTTTCTGTAAGAAATAT 1540
Db 492 GTGTTATGGGATCTAGTGAATATATGAAAGTCTTTTCTGTAAGAAATAT 551
QY 1541 GTATGAGAGTTTCATCTTTTCAATAGTGAACAACTCTCTTTCATACCAAAAAAAT 1600
Db 552 GATCACTAAGAGCGTCTTATTTATGAGAAACAATCTTTTTCATACCAAAAAAAT 611
QY 1601 TTGAAAAAATTTAGTGAACCTCTCTTTGCGATTTAGTGTGAGTTCAGATCA 1660
Db 612 TGGAGAAAAATTCGGGAAACCTTTTTCGCGTTTGGAGGGTTGGCCCAATTC 671
QY 1661 AATACGATAGCATACAAATTTTGGCATGCGCAATTTGTCGAGGTAAATATA 1720
Db 672 AA--GCCAATACCTTACCTTTTTCGCGTGAATCTATGCGTTCGGGGAAATTA 729
QY 1721 CCAATAGAAACATATTTTGGAGTAGTTAAGATTATGATGAAGAAATCTATTACGAT 1780
Db 730 CCACTTGGACATTTTNAAGAGCTATTCAGATTTGATGGAAGAA-----TCTTTTCGG 786
QY 1781 AAGCATAAATTTCTTTGCTGTTCTTTGTTTCTGTTTATGAGACATGTAATG 1840
Db 787 ATGGCATAACTTTCTTTGCGGACCTGGTTTTCGCGCTTTTA---AAACATGAAAG 843
QY 1841 TACTTTGTTTTCACCATAGATATGATGATACATACATAGTAAGTACGATG 1900
Db 844 CACTTTGCTTTTTCGCGGCTTTTTCGCGCTTTTTCGCGCTTTTTCGCGCTTTT 903
QY 1901 TTATATAGAGAGATTT 1918
Db 904 TTCAAAGGAAATGTTTT 921
```

```
RESULT 7
BZ35348 323 bp DNA linear GSS 14-NOV-2002
LOCUS SALK_126660.22.95.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_126660.22.95.x; genomic
survey sequence.
ACCESSION BZ35348
KEYWORDS BZ35348.1 GI:24946361
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 323)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
```

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 323
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clones="SALK_126660.22.95.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 12.6%; Score 256; DB 8; Length 323;
Best Local Similarity 88.9%; Pred. No. 3.8e-34;
Matches 288; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
QY 1690 CATGCCAATTATTGTCGAGGTAAATATACCAATAGAAACATATTTTAGGAGTAGTT 1749
Db 1 CATGGAATATTCTCTGGGTAAATATCCATTAGAAACTTCTTTGGGGAGCATTT 60
QY 1750 AAGATTATGTTGAAGAAATCTATTACGATAGCATAAATTTCTTTGCTGTTG 1809
Db 61 AAAATTATGATTGAAGAGATTTCTTTTACGATAGGCTTGCAATTTCTTTGCTGCTCG 120
QY 1810 GTTTTTCGTTTATAGAACATTCGAATATGATGTTTGTGTTTTCACCAAGTAGATAT 1869
Db 121 GTTTTTCGTTTATAGAACATTCGAATATGATGTTTGTGTTTTCACCAAGTAGATAT 180
QY 1870 GTACTATACACATAGTAACATCGGTAGTTTATATAGAGAGATTTGATTTTCGTA 1929
Db 181 GTTCTATACCCATAGTAACATCGGTAGTTTATATAGAGAGATTTGATTTTCGTA 240
QY 1930 TATTTCTTTTGTGAAATAAATATGTTGTAATAATTTATTTTATTTTACACATTT 1989
Db 241 TATTTCTTTTGTGAAATAAATATGTTGTAATAATTTATTTTATTTTATTTTACACATTT 299
QY 1990 GTTCAGTTGAGAGTTTAAATTA 2013
Db 300 GTTCCCTCGGAAAGTTTAAATTA 323

RESULT 8

BZ35348

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

BH09771 246 bp DNA linear GSS 02-MAY-2002
SALK_005656 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_005656; genomic survey sequence.
BH09771
BH09771.1 GI:20387588
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 246)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At4g20250.

Class: TDNA tagged.

Location/Qualifiers

1. .246

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_005656"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html."

FEATURES

source

1. .246

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_005656"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html."

ORIGIN

Query Match

Best Local Similarity 11.3%; Score 230; DB 8; Length 246;

Matches 236; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 855 TCCTCTTCTGTTTCCACCGTTAAATTCAAATTTTACTATTGTTACCGCTGCTTTTACCTTTT 914

Db 1 TCCTCGTCTGTTTCCACCGTTAAATTCAAATTTTACTATTGTTACCGCTGCTTTTACCTTTT 60

Qy 915 TTAAGAAACCCCAACCCGAATATACATATACCGAATACATGCTTCTTACGTGACGT 974

Db 61 TTAAGAAACCCCAACCCGAATATACATATACCGAATACATGCTTCTTACGTGACGT 120

Qy 975 AACAAAGCTTATTTTCCGGTTGAATTTGGTTTAACTATTGAGATTGCTTAAACGAAAA 1034

Db 121 AACAAAGCTTATTTTCCGGTTGAATTTGGTTTAACTATTGAGATTGCTTAAACGAAAA 180

Qy 1035 CAGAAACGGTTATGACGCCAACGAGGCAAGAGGGGTAAACGAGAAAGAGGGGATGGCAG 1094

Db 181 CCGAAGCGGTTATGACGCTCACCGGCAAGAGGGGCAAAACGAGAAAGGGGATGGCCG 240

Qy 1095 AAATCG 1100

Db 241 AAATCG 246

RESULT 9

BZ062372

LOCUS 11e85b02.b1 B.oleracea002 Brassica oleracea genomic, genomic survey

DEFINITION 749 bp DNA linear GSS 10-OCT-2002

sequence.

ACCESSION BZ062372

VERSION BZ062372.1 GI:23672357

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 749)

Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@wustl.edu

Plate: 11e85 row: b column: 02

Seq primer: -21UPpOT forward

Class: shotgun

High quality sequence start: 21

High quality sequence stop: 551.

Location/Qualifiers

1. .749

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/notes="Vector: pOTw13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea T0100DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

ORIGIN

Query Match

Best Local Similarity 7.7%; Score 156.6; DB 8; Length 749;

Matches 424; Conservative 0; Mismatches 159; Indels 52; Gaps 12;

Qy 722 ATGTTCAACTACAGATCACCATCCCAATTAACAATCCGATTTGGTCGGGCCCACTGTTT 781

Db 32 ATTTCTACCCCTATAGATTACCATCTAATAATAACAATCCCATTTGGTACGGGACCTACTTT 91

Qy 782 CGATATTTGCCAACTGTGATTGTGACGTGCAGCTGCCAGTGGCATATTTTCCCTCTCGATTA 841

Db 92 -GATCTTTGCCAACTCTGTTTGATGTGACCGCAGCTGGCATATTTCCATCTTAAATTTA 150

Qy 842 CGTTT-----TTACCCCTTCTCTCTTCTTCCCGTTTAACTTCAATTTTACTATTT 892

Db 151 TGTTACCCCTTGCCATCTCGGTCCTCTCTGTTTGACAGTTATTTCCAATATT-TAACTT 209

Qy 893 GTACCGGTGCTTTTACCC-----TTTTTAAGAAAAACCCCAACCCGGAATCATTAAC 943

Db 210 GTACTGCTGCTCTGACCCATTTCCGGTTATCGAAGAAAAATCAGAACTAAATACACAGT 269

Qy 944 ATACCGAAATCACATGCTTCA-----TGGTGACGTAAACAAGACTTTATTTTCGG 993

Db 270 ATTCGGAACCGGTTTACATAAAACCATGGATGGATGATGTTTGAAGAGTATTTTCGGT 329

Qy 994 TTGAATTTGGTTTAAACCTATTGGAGATTGTGCTAACCGAAAAACAGAAACGGTTATGACGCC 1053

Db 330 TTAATGTTGCTTAATTGAGGAGATAACCGCGAAGAGACGACAGAAAAACGGTTAAGATGCC 389

Qy 1054 AA-CGAGGCAAGAGGGGTAAAAACGAGAAAGAGGGGATGGCAGAAATCGTAATTAACAAG 1112

Db 390 AATTGAGGCAAGAGGGGTAA-----AGAAGAGAGAGGGGGTCAATATTCGTAAATTAAGAAG- 444

Qy 1113 AAATAAAGGGTGGTTTTCAGATAAGTCTCTATATATGACGCGAAAGGGTTTCTTAAATT 1172

Db 445 AAACAAGGGGTGATTTTGAAGAGAACCATATCTATATGACGTGAAGGGTT-----TT 497

Qy 1173 CAGAGAGACAAATTAATCAGTTTTCGTGTGTTT-GGAGAAAGAAAGAAAGACAGATCAAAATCG 1231

Db 498 CAGAGAAACAAATTAATCAGTTTTCGTGTGTTTCAAAGAAAGAAAGAAAGACAGATCGA----- 552

Qy 1232 AGGAGAGATCTTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTAAT- 1290

Db 553 GACGAGATCTCGAAAGAGATTTTATCATCTCAAGTAAGTTTCTATATCAAACTCGTGATG 612

Qy 1291 --ATAACAATCAAAACATGAACACGCTCGTGCT 1323

Db 613 AAATTAACAATCAAAACATGAATGTGTTTTT 647

RESULT 10

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BH439107/C
LOCUS BH439107 713 bp DNA linear GSS 12-DEC-2001
DEFINITION BOHAK61TR BOHA Brassica oleracea genomic clone BOHAK61, genomic
survey sequence.
ACCESSION BH439107
VERSION BH439107.1 GI:17624821
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
PUBMED 1 (bases 1 to 713)
REFERENCE Whole genome shotgun sequencing of Brassica oleracea
AUTHORS Unpublished (2001)
TITLE Other GSSs: BOHAK61TF
JOURNAL Contact: Chris Town
COMMENT TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
location/Qualifiers
1..713
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone_lib="BOHAK61"
/clone="BOHAK61"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN
Query Match 7.2%; Score 147; DB 8; Length 713;
Best Local Similarity 68.9%; Pred. No. 2.1e-15;
Matches 224; Conservative 0; Mismatches 85; Indels 16; Gaps 1;
QY 966 TGGTGCAGTAACAAGACTTATTTTCGGTTGTAATTTGGTTTAACTTATTGAGATTGTGCT 1025
DB 454 TGGTTCTTAGGTTTAAGTTTGTGTTGATGTCATGAGAAAGTTGTAACCGAATTTGCC 395
QY 1026 AACCGAAAACAGAAACGGTTATGACGCCAACGAGGCAAGAGGGGTAAACCGAAGAGG 1085
DB 394 GCGAAGAGACGAAACGGTTAAGACTCCCAACGAGCGGAGGGGTAATACGAGAAAAGAG 335
QY 1086 GGATGCGAANAATCGTAATATACAGGAAATTAAGGGTGGTTTCAGATAAGTCTGTCT 1145
DB 334 CGAGGGCAAGAATCGTAATTAATTAAGAAAGCCAAAGGGTGAATTGAAGAGAAACCTGTCT 275
QY 1146 ATATGACGCGAAGGGTTCTTAAATTCAGAGACAATTAATCACTTTTCGTGTGTTGG 1205
DB 274 ATATGACGCGTAAGTGTCTTAAATTCAGAGACAATTAATCACTTTTCGTGTGTTCA 215
QY 1206 AGAAGAAGAAAGACAGATCAATCAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAG 1265
DB 214 GAGAAGAAAGAGAG-----GATCTCAAGAGAGATTATCATCTCAAG 171
QY 1266 TAAGTCTCTTTATCAAACTCTTAAT 1290
DB 170 TAAGTCTCTTTACCAAACTCATAGT 146
RESULT 11
CR402809
LOCUS CR402809 194 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-858C06-025968,
genomic survey sequence.
ACCESSION CR402809

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VERSION CR402809.1 GI:46943537
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.
PUBMED 1 (bases 1 to 194)
REFERENCE Arabidopsis thaliana T-DNA insertion mutants in Arabidopsis
AUTHORS thaliana
TITLE Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL 22755829
PUBMED 12874060
REFERENCE Arabidopsis thaliana T-DNA insertion mutants in Arabidopsis
AUTHORS Weissshaar, B.
TITLE Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
JOURNAL An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
PUBMED flanking sequence tag-based reverse genetics
AUTHORS Plant Mol. Biol. 53 (1-2), 247-259 (2003)
TITLE 23117147
JOURNAL 14756321
PUBMED 14756321
REFERENCE Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
TITLE Weissshaar, B.
JOURNAL High-throughput generation of sequence indexes from T-DNA
PUBMED Arabidopsis thaliana lines
AUTHORS Biotechniques 35 (6), 1164-1168 (2003)
TITLE 14682050
JOURNAL 14682050
PUBMED 14682050
REFERENCE Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weissshaar, B.
TITLE Direct Substitution
JOURNAL Submitted (01-MAY-2004) Weissshaar B., Max-Planck-Institut fuer
PUBMED Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
AUTHORS This sequence has been recovered from the left border of the T-DNA.
TITLE It indicates an insertion close to or within gene At4g20250.
JOURNAL Details on the protocols used for generation of the sequence are
PUBMED described in References 1-3. The sequences are generated at the MPI
AUTHORS for Plant Breeding Research in the context of the GABI-Kat project.
FEATURES GABI-Kat is part of the German Plant Genomics program designated
location/Qualifiers
1..194
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."
ORIGIN
Query Match 6.6%; Score 134.8; DB 9; Length 194;
Best Local Similarity 84.8%; Pred. No. 3e-13;
Matches 151; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 718 GTATATGTTTACAACTACAGATCACCATCCACAAATTAAACATTCGATTGTGGGGGCATT 777
DB 17 GAATATATATTGAATATATATACGTTGATTATTAATTAATTAATTAATTAATTAATTAAT 76
QY 778 GTTTCGATATTTGCCAACTGTGATTGATGTGACTGCAGCTGCATATTTTCCCTCCCTG 837
DB 77 GTTTCATATTTGCCAACTGTGATTGATGTGACTGCAGCTGCATATTTTCCCTCCCTG 136

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Qy 838 ATTACGTTTTTACCGTTTCCTCTCTGTTTCCACCGTTAAATCAATTTTACTATTGTA 895
Db 137 ATTACGTTTTTACCGTTTCCTCTCTGTTTCCACCGTTAAATCAATTTTACTATTGTA 194

RESULT 12
BH745927/c
LOCUS 597 bp DNA linear GSS 25-FEB-2002
DEFINITION g274a08.b1 BoBuds01 Brassica oleracea genomic clone g274a08 5',
genomic survey sequence.
ACCESSION BH745927
VERSION BH745927.1 GI:18880776
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 597)
AUTHORS Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J.,
Belija,V., Cunniss,D.M., Katzenberger,F., King,L., Kirchoff,K.,
Kuit,K., Miller,B., Muller,S., Nascimento,L., Preston,R.,
Santos,L., Shah,R., Zutavern,T., Dedhia,N., Rabinowicz,P.D. and
McCombie,W.R.
TITLE Whole Genome Shotgun Reads from Brassica oleracea (2002b)
COMMENT Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: g274 row: a column: 08
Seq primer: -21UnivFwd
Class: shotgun
High quality sequence stop: 597.
FEATURES
source
Location/Qualifiers
1..597
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone="g274a08"
/clone_lib="BoBuds01"
/notes="Vector: M13 for .x reads, pBluescript for .b and .g
reads; Site 1: EcoRV; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear prep
using Brassica oleracea TO1000DH3 buds provided by Thomas
Osborn at the University of Wisconsin. Genomic DNA
provided by Pablo Rabinowicz (CSHL) and shotgun library
prepared in McCombie Lab."

ORIGIN
Query Match 6.4%; Score 130; DB 8; Length 597;
Best Local Similarity 65.1%; Pred. No. 1.8e-12;
Matches 242; Conservative 0; Mismatches 120; Indels 10; Gaps 3;

Qy 553 AAATTTAATCGAGGATAATCAATATCCAACTCAACGATAATCAAAAGCCTAATAATAGAT 612
Db 542 AAGTCCAACTACATTTTTCAGATTTTCGAGGATAATCAATAATCCAACTCAAAATGATGACAT 483

Qy 613 CA--ATGAAATCAATAACTAAACATAGTATATATACATTTGTTGTATAACAGATAA 670
Db 482 TAACATCAATGGAAATAATCAAAAACAGATAATAATAAGGTCGTGATCTCTTAAACAGATAA 423

Qy 671 TATACATTATAATAG-----TATGAAATATCAATATAATAGATAAGAGCGGTATAT 723
Db 422 TATACATTATATATAGAAATTTTGTATATATTAGATAAGATCAATAGATGCGTATAT 363

Qy 724 GTTACAACTACAGATCACCATCCACAATTAAACAATCCGATTGGTCCGGGCCAATTGTTTCG 783
Db 362 GTTACACCTACAGATCACCATCCAGAAATTAACAATCCGATTGGTCCGGGCTCTACTTT-G 304

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Qy 784 ATATTTGCCAACTGTGATTGACTGCGAGTCCGACATATTTCCCTCCTGATTACG 843
Db 303 ATATTTGCCAACTGTAAATTGATGACCGCCAGTCCGCAAATTTTGTCTGAAATTACCT 244

Qy 844 TTTTACCTTTCTCTCTTCTGTTTCAACGTTAAATTTCAATTTTACTATTGTACCGCTGTC 903
Db 243 ATTTGCCCTTTTCAACTCTCTGTTTCGACCGTTATTTCTGTTTGTACTTGGCTGCTGTC 184

Qy 904 TTTACACCTTTT 915
Db 183 ATTGACCCCTTT 172

RESULT 13
CL489509/c
LOCUS 982 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL 525 C07.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_525_C07.v1, genomic survey sequence.
ACCESSION CL489509
VERSION CL489509.1 GI:45971813
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 982)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kinnerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS822250; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: T-DNA tagged.
FEATURES
source
Location/Qualifiers
1..982
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL 525_C07.v1"
/clone_lib="SAIL Collection"
/notes="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match 6.2%; Score 125.2; DB 9; Length 982;
Best Local Similarity 91.1%; Pred. No. 1.2e-11;
Matches 133; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1197 TGTGTTTGGAGAGAAGAAACAGATCAATACGAGAGAGATCTCTTAAGAGATTAT 1256
Db 196 TGTGCTGGGGTGTGAAGAGACACAGATCAATACGAGAGAGATCTCTTAAGAGATTAT 137

Qy 1257 CGTTTCAAGTAAGTCTCTTTTATCAAACTTTAATATAAAACAAATCAAAACATGAACAGT 1316
Db 136 CGTTTCAAGTAAGTCTCTTTTATCAAACTTTAATATAAAACAAATCAAAACATGAACAGT 77

Qy 1317 CGTGTCTTCGTTTCGATTCTTAGATAC 1342
Db 76 CGTGTCTTCGTTTCGATTCTAACAAC 51

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RESULT 14
BH425990/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH425990
BOGJF07TR BOGJ Brassica oleracea genomic clone BOGJF07, genomic survey sequence.
BH425990
BH425990.1 GI:17611718
GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 786)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGJF07TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: Sheared ends.

FEATURES
source
Location/Qualifiers
1..786
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGJF07"
/clone_lib="BOGJ"
/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN
Query Match 5.9%; Score 119.6; DB 8; Length 786;
Best Local Similarity 67.5%; Pred. No. 1.1e-10;
Matches 216; Conservative 0; Mismatches 94; Indels 10; Gaps 3;

QY 553 AAATTAAATCGAGGATAATCAATATCCAACTCAACGATAATCAAAAGCCTAATAATAGAT 612
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Db 319 AAGTCMAACTACATTTTCAGATTTTCGAGGATAATCATATCCAACTCAAGATATGACAT 260
|||
QY 613 CA--ATGAATCAATAACTTAACATAGTAGTAATACATTTGATTTGTTAAACAGATAAA 670
|||
Db 259 TAACATCAATGAATAATCAAAACAGAAATATATAGGTCGTGATGCTTTAAACAGATAAA 200
|||
QY 671 TATACATTATAATAG-----TATGAAATATGAATATAATAGATAAGAGCGGTATAT 723
|||
Db 199 TATACATTATAATATGAATTTTGTATATATAGATAAGATCATAGATGCGTATAT 140
|||
QY 724 GTTAACTACAGATCACCATCCACATTAACAAATCCGATTTGGTGGGCGCAATTTGTTTCG 783
|||
Db 139 GTTACACCTACAGATCACCATCCAGAAATTAACAAATCCGATTTGGTGGGCTCTACTTT-G 81
|||
QY 784 ATATTGCCAACTGCTGATGATGCTGCCAGCTGGCATATTTTCCCTCCCTGATTAG 843
|||
Db 80 ATATTGCCAACTGCTGATGATGCTGCCAGCTGGCAATTTTGTCTGAAATTTACCT 21
|||
QY 844 TTTTACCCTTTCTCTCT 863
|||
Db 20 ATTGGCCCTTTCAACTCCT 1
|||

RESULT 15
CG750135/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

P044-3-D09.za Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
CG750135
CG750135.1 GI:37971278
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1592)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
12884007
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES
source
Location/Qualifiers
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN
Query Match 4.6%; Score 93.6; DB 9; Length 1592;
Best Local Similarity 45.0%; Pred. No. 3.2e-06;
Matches 412; Conservative 0; Mismatches 495; Indels 9; Gaps 4;

QY 5 ATAGAAGATGACCATTTGAAGAATACCTTCCTCTTTCTATTTTATTTGATTAGAAA 64
|||
Db 1313 ATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1254
|||
QY 65 TCATATTCATTCACAAAGCAAAATAATAATTTTGTATCCTAAAGCTTAACTTAC 124
|||
Db 1253 TTATNTTTAAATATATTTTATATATTTTAAANAAATTAATAATAATAATAATAATA 1194
|||
QY 125 AATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGGTTTT 184
|||
Db 1193 ATTAATAATNTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1134
|||
QY 185 AGGAAAAATGATCTCTTTTCATATAAAAAATATATAGATCTTCAAGAACTGAATGGGT 244
|||
Db 1133 AAATATAAAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1076
|||
QY 245 TTTCAACTATTTTATCGTTTGACACTCTTTGACCTTATCAAAAGAGTTCAAAATAGAA- 303
|||
Db 1075 TNATAAATAATTTAAATTTTATATATTTAAATNATATATTTAAANAAATTAATAATA 1016
|||
QY 304 --AAATAGAAATCGAATCACACCGTTTCAGTGTGAAGAGGATTTTGATATTTGGTCA 361
|||
Db 1015 ATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 956
|||
QY 362 AAAGAGTTGTTTGTGTTTTTTTTTCCAACTCGCATGGTTTTTTCGTCGTTGAACCAAT 421
|||
Db 955 ATAAATAATAATTTNTATATTTATTTATTTATTTTNTAAAAATTAATAATAATAATA 896
|||
QY 422 CAACACTTTGTATAAACCGAATAGTAATATCTAGACGTACGCCAATACCAAAAAATAAA 481
|||
Db 895 TAATAATAAAAAATTTAAATAAATNTTATAATAATAATAATAATAATAATAATAATA 836
|||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: October 23, 2005, 22:24:33 ; Search time 8753 Seconds
(without alignments)
11237.757 Million cell updates/sec

Title: US-10-643-676-1
Perfect score: 2030
Sequence: 1 cttcagaagatggacca.....ttagattaaacaacaaaag 2030

Scoring table: OIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_ey.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030	100.0	2030	6	AX548023 Sequence
2	2030	100.0	2042	6	AX548024 Sequence
3	2030	100.0	11945	8	ATFIC12 Arabidops
4	2030	100.0	198427	8	ATCHRIV52 Arabidops
5	1064	52.4	1064	6	AX509457 Sequence
6	209	10.3	288	11	AL807890 Arabidops
7	209	10.3	290	11	BX295033 Arabidops
8	91	4.5	1001	8	AY086004 Arabidops
9	79	3.9	1070	8	AY093084 Arabidops
10	74	3.6	1105	8	ATENDASPR Arabidops
11	58	2.9	604	8	AF083669 Arabidops
12	25	1.2	11126	9	AF321237 Homo sapi
13	25	1.2	171660	9	AC017103 Homo sapi
14	25	1.2	173611	9	AC087280 Homo sapi
15	25	1.2	208430	2	AC027641 Homo sapi
16	25	1.2	211735	9	AC091564 Homo sapi
17	25	1.2	349980	6	AX344555 Sequence
18	24	1.2	495	4	AF421477 Canis fam
19	24	1.2	1362	5	BC073620 Xenopus 1

AF106580 Caenorhab
AC109320 Homo sapi
AC105258 Oryza sat
AC106033 Homo sapi
Continuation (2 of
AL020985 Caenorhab
Continuation (19 o
AL132858 Caenorhab
AC147100 Pan trogl
CR118611 Danio rer
AC105247 Homo sapi
AC021145 Homo sapi
AC146114 Pan trogl
AC074567 Pan trogl
AC074269 Homo sapi
AL158069 Human DNA
AC002385 Homo sapi
AC146375 Pan trogl
AF232704 Bos tauru
AX835236 Sequence
AK098176 Homo sapi
Z83241 Caenorhabdi
AL021175 Caenorhab
AC149380 Phakopso
AL008866 Caenorhab
AC024792 Caenorhab
AF198095 Homo sapi
AC108921 Homo sapi
AC129535 Mus muscu
AC074084 Homo sapi
AL451131 Human DNA
AC125481 Medicago
AP003910 Oryza sat
AC087698 Homo sapi
AP004566 Oryza sat
AC003564 Oryza sat
AC116551 Dictyoste
BX248384 Zebraphish
AC083934 Homo sapi
Z98551 Plasmodium
AC007994 Mus muscu
AC150964 Bos tauru
AC090151 Homo sapi
AC012461 Homo sapi
BX469917 Danio rer
AC144748 Pan trogl
AC120600 Rattus no
AL513406 Human DNA
AC125367 Rattus no
AC096612 Rattus no
AC108960 Rattus no
CR318600 Danio rer
AC094412 Rattus no
AC127711 Rattus no
AC006785 Caenorhab
CQ528967 Sequence
BV070459 S212P6018
AJ334130 Homo sapi
U73685 Dictyosteai
AF118151 Dictyoste
X71020 N.kabacum N
Y53237 D. discoide
AY254473 Dictyoste
AY160096 Dictyoste
CQ788989 Sequence
AR218848 Sequence
BD003760 Polynucle
AF269225 Cloning v
AF269226 Cloning v
AE008407 Streptoco
AE007341 Streptoco
AF269238 Cloning v
AF269237 Cloning v

c	93	22	1.1	11335	12	AF270470	166	22	1.1	183648	3	AC117081	AC117081 Dictyoste
	94	22	1.1	13674	3	U00691	c 167	22	1.1	186675	5	AL845306	AL845306 Zebrafish
	95	22	1.1	13729	3	U00796	c 168	22	1.1	188557	1	EX248586	EX248586 Blochmann
c	96	22	1.1	21494	3	CEY17D7A	169	22	1.1	188972	2	AC006907	AC006907 Caenorhab
	97	22	1.1	36188	3	AC116922	c 170	22	1.1	198823	10	AC121598	AC121598 Mus muscu
	98	22	1.1	38591	1	CBC5AE10	c 171	22	1.1	190149	9	AC146127	AC146127 Pan trogl
	99	22	1.1	39575	3	AC116925	c 172	22	1.1	190323	2	AX004881	AX004881 Danio rer
	100	22	1.1	39916	3	U42848	c 173	22	1.1	191909	9	AP002810	AP002810 Homo sapi
c	101	22	1.1	39935	3	AF016662	c 174	22	1.1	191988	2	CR388129	CR388129 Danio rer
c	102	22	1.1	40803	3	CEC11E4	c 175	22	1.1	195346	2	AC148248	AC148248 Ocolemur
c	103	22	1.1	41131	3	AF038609	176	22	1.1	198781	9	AC012046	AC012046 Homo sapi
	104	22	1.1	41869	3	CEY51H1A	c 177	22	1.1	200761	10	AC122140	AC122140 Mus muscu
	105	22	1.1	43666	3	CEY51H1A	c 178	22	1.1	201070	5	AX004830	AX004830 Zebrafish
c	106	22	1.1	44264	3	CEC47D12	c 179	22	1.1	203476	2	AC074150	AC074150 Mus muscu
c	107	22	1.1	59573	3	CEY45F10D	c 180	22	1.1	203699	2	AC040973	AC040973 Homo sapi
c	108	22	1.1	67416	2	AC115955	181	22	1.1	204147	2	AC145056	AC145056 Danio rer
c	109	22	1.1	71225	9	AL358196	c 182	22	1.1	205954	2	AC118829	AC118829 Rattus no
c	110	22	1.1	71225	9	AL358196	c 183	22	1.1	208066	9	AC146483	AC146483 Pan trogl
c	111	22	1.1	79980	2	AC137927	c 184	22	1.1	213456	2	CR628368	CR628368 Danio rer
c	112	22	1.1	85916	3	AC117080	c 185	22	1.1	215502	2	CR749161	CR749161 Danio rer
c	113	22	1.1	89249	3	AC103567	c 186	22	1.1	217249	10	AL663095	AL663095 Mouse DNA
c	114	22	1.1	92176	2	AC022961	187	22	1.1	218657	10	AC110517	AC110517 Mus muscu
c	115	22	1.1	93177	9	AC098678	c 188	22	1.1	221050	2	AC096854	AC096854 Canis fam
c	116	22	1.1	102867	8	ATAC011436	c 189	22	1.1	221583	2	AC140756	AC140756 Rattus no
c	117	22	1.1	106688	8	ATAC011436	c 190	22	1.1	223624	2	AC126845	AC126845 Rattus no
c	118	22	1.1	110000	2	AC1091367_4	c 191	22	1.1	239328	2	AC123494	AC123494 Rattus no
c	119	22	1.1	110000	2	AC106988_0	c 192	22	1.1	240103	2	AC111794	AC111794 Rattus no
c	120	22	1.1	110000	3	AC116305_0	c 193	22	1.1	243122	2	AC134020	AC134020 Rattus no
c	121	22	1.1	110000	8	AC116984_0	194	22	1.1	243235	2	CR318614	CR318614 Danio rer
c	122	22	1.1	110000	8	CR380957_05	195	22	1.1	243851	2	AC123448	AC123448 Rattus no
c	123	22	1.1	110000	8	CR380957_06	196	22	1.1	248077	2	AC112366	AC112366 Rattus no
c	124	22	1.1	112222	2	AC007764	c 197	22	1.1	250195	3	AE014831	AE014831 Plasmodiu
c	125	22	1.1	119825	2	AC148342	c 198	22	1.1	251780	2	AC130912	AC130912 Rattus no
c	126	22	1.1	120846	9	AC018356	c 199	22	1.1	253985	2	AC123321	AC123321 Rattus no
c	127	22	1.1	125623	3	AC115599	c 200	22	1.1	293183	2	AC095903	AC095903 Rattus no
c	128	22	1.1	125970	2	AC136841	c 201	22	1.1	293218	2	AC128441	AC128441 Rattus no
c	129	22	1.1	127307	2	AC151398	c 202	22	1.1	298406	3	CEY75B8A	CEY75B8A Caenorhab
c	130	22	1.1	132254	3	AC118330	c 203	22	1.1	312430	1	RPX002	RPX002 Rickettsi
c	131	22	1.1	132715	5	AX465189	c 204	22	1.1	321304	3	CEY105C5B	CEY105C5B Caenorhab
c	132	22	1.1	133924	5	AC093712	c 205	22	1.1	331039	3	AC116979	AC116979 Dictyoste
c	133	22	1.1	136804	9	AP000469	c 206	22	1.1	340000	9	AP001689	AP001689 Homo sapi
c	134	22	1.1	137858	2	AC151397	c 207	22	1.1	349980	6	AX571760	AX571760 Sequence
c	135	22	1.1	139627	9	AL357117	c 208	22	1.1	132	14	HPA277788	HPA277788 Human pap
c	136	22	1.1	142506	2	CR678304	c 209	21	1.0	374	6	CO407892	CO407892 Sequence
c	137	22	1.1	143137	5	AX004865	c 210	21	1.0	549	6	CO410381	CO410381 Sequence
c	138	22	1.1	143138	5	AL954181	c 211	21	1.0	555	8	AJ841026	AJ841026 Arabidops
c	139	22	1.1	146570	6	AC117076	c 212	21	1.0	622	6	CO427774	CO427774 Sequence
c	140	22	1.1	149634	9	AC113172	c 213	21	1.0	704	3	AY617813	AY617813 Sterkiell
c	141	22	1.1	149990	10	AC122803	c 214	21	1.0	1435	4	S74436	S74436 OIL-8-inter
c	142	22	1.1	151727	2	AC006894	c 215	21	1.0	1494	4	OAIL8	OAIL8 O.aries int
c	143	22	1.1	156221	2	AC134963	c 216	21	1.0	1618	3	CEU55018	CEU55018 Caenorhabdi
c	144	22	1.1	156372	5	BX072531	c 217	21	1.0	2267	6	AR217142	AR217142 Sequence
c	145	22	1.1	157314	2	CR352289	c 218	21	1.0	2267	6	AX206706	AX206706 Sequence
c	146	22	1.1	157847	10	AC122511	c 219	21	1.0	2267	10	MUSFISP12B	MUSFISP12B M70642 Mouse FISP-
c	147	22	1.1	159243	2	AC135660	c 220	21	1.0	2334	6	BC006783	BC006783 Mus muscu
c	148	22	1.1	159647	5	EX897658	c 221	21	1.0	2338	6	E37595	E37595 Monoclonal
c	149	22	1.1	160557	2	CR759918	c 222	21	1.0	2338	6	AR317175	AR317175 Sequence
c	150	22	1.1	162139	9	AC005682	c 223	21	1.0	2338	10	AB023068	AB023068 Rattus no
c	151	22	1.1	162797	2	AC023219	c 224	21	1.0	2350	6	BD242736	BD242736 Connectiv
c	152	22	1.1	168363	10	AL713917	c 225	21	1.0	2350	6	AR194011	AR194011 Sequence
c	153	22	1.1	168910	5	CNS098BV	c 226	21	1.0	2350	6	AR201286	AR201286 Sequence
c	154	22	1.1	169168	5	EX890629	c 227	21	1.0	2469	8	SCU02598	SCU02598 Saccharomyc
c	155	22	1.1	169604	2	EX640595	c 228	21	1.0	2766	10	BC072503	BC072503 Rattus no
c	156	22	1.1	175345	2	AC022301	c 229	21	1.0	2957	8	YSCVPS16P	YSCVPS16P Rattus no
c	157	22	1.1	175527	2	AC107745	c 230	21	1.0	3041	5	AB005553	AB005553 Gallus ga
c	158	22	1.1	175936	2	SPNEU1908	c 231	21	1.0	3065	8	SCNQP77	SCNQP77 X76245 S.cerevisia
c	159	22	1.1	177166	2	AC123979	c 232	21	1.0	5307	6	AX348430	AX348430 Sequence
c	160	22	1.1	178534	2	AC027203	c 233	21	1.0	5307	6	AX348825	AX348825 Sequence
c	161	22	1.1	179724	9	AP003094	c 234	21	1.0	5725	3	AF482384	AF482384 Dictyoste
c	162	22	1.1	181230	5	EX296556	c 235	21	1.0	6204	6	AX346729	AX346729 Sequence
c	163	22	1.1	182871	3	AC117176	c 236	21	1.0	6207	6	AX251536	AX251536 Sequence
c	164	22	1.1	182871	3	AC117176	c 237	21	1.0	6821	2	AC017404	AC017404 Drosophil
c	165	22	1.1	183137	2	CR759797	c 238	21	1.0	7644	8	TAU51303	TAU51303 Triticum ae

C 239	21	1.0	9357	6	AX251403	AX251403 Sequence	C 312	21	1.0	110191	3	AC087255	AC087255 Caenorhab
C 240	21	1.0	10425	6	CQ607523	CQ607523 Sequence	C 313	21	1.0	112512	2	AP003744	AP003744 Oryza sat
C 241	21	1.0	14095	6	AX345378	AX345378 Sequence	C 314	21	1.0	114505	8	F20P5	F20P5 Sequence
C 242	21	1.0	14644	9	HSBTKS4	HSBTKS4 Sequence	C 315	21	1.0	114534	5	BX294117	BX294117 Zebrafish
C 243	21	1.0	17070	8	AB001916	AB001916 Oryza sat	C 316	21	1.0	119238	8	AC137064	AC137064 Oryza sat
C 244	21	1.0	24942	3	CEK03D3	CEK03D3 Zebrafish	C 317	21	1.0	119745	8	AC141108	AC141108 Medicago
C 245	21	1.0	2520	3	AF099918	AF099918 Caenorhab	C 318	21	1.0	120743	8	AP004082	AP004082 Oryza sat
C 246	21	1.0	32847	3	AF025460	AF025460 Caenorhab	C 319	21	1.0	120926	2	AC133008	AC133008 Oryza sat
C 247	21	1.0	33038	3	CEY668	CEY668 Caenorhab	C 320	21	1.0	122479	3	CEY113G7A	CEY113G7A Caenorhab
C 248	21	1.0	33858	8	SCU44030	SCU44030 Saccharomyc	C 321	21	1.0	122715	10	AL845335	AL845335 Mouse DNA
C 249	21	1.0	36075	5	AF025468	AF025468 Caenorhab	C 322	21	1.0	122770	8	AC147007	AC147007 Medicago
C 250	21	1.0	36348	3	AC024765	AC024765 Caenorhab	C 323	21	1.0	123091	3	AC1787G2A	AC1787G2A Caenorhab
C 251	21	1.0	36865	3	AF099896	AF099896 Caenorhab	C 324	21	1.0	123623	2	CEY151084	CEY151084 Bos tauru
C 252	21	1.0	36865	3	AF099896	AF099896 Caenorhab	C 325	21	1.0	127883	10	AC114434	AC114434 Rattus no
C 253	21	1.0	37663	3	AF036699	AF036699 Caenorhab	C 326	21	1.0	127883	8	AP003118	AP003118 Oryza sat
C 254	21	1.0	43764	3	AF016672	AF016672 Caenorhab	C 327	21	1.0	129441	9	AL136170	AL136170 Human DNA
C 255	21	1.0	44364	3	AC091125	AC091125 Caenorhab	C 328	21	1.0	129461	2	CR677748	CR677748 Danio rer
C 256	21	1.0	44375	9	AC148448	AC148448 Pan trogl	C 329	21	1.0	131182	10	AC132259	AC132259 Mus muscu
C 257	21	1.0	44690	2	AC138022	AC138022 Botryllus	C 330	21	1.0	131741	8	AP004916	AP004916 Lotus cor
C 258	21	1.0	48891	8	AC082643	AC082643 Arabidops	C 331	21	1.0	132445	4	AY152826	AY152826 Felis cat
C 259	21	1.0	54441	3	AC115584	AC115584 Dictyoste	C 332	21	1.0	132906	2	AC145218	AC145218 Medicago
C 260	21	1.0	57538	3	AC115682	AC115682 Dictyoste	C 333	21	1.0	133197	2	AC146703	AC146703 Medicago
C 261	21	1.0	67374	9	CR394533	CR394533 Human DNA	C 334	21	1.0	133406	3	AF321227	AF321227 Tribolium
C 262	21	1.0	67392	9	AC034250	AC034250 Homo sapi	C 335	21	1.0	133575	8	CNS08C9N	CNS08C9N Oryza sat
C 263	21	1.0	68143	9	AC034250	AC034250 Homo sapi	C 336	21	1.0	134825	8	AC099325	AC099325 Oryza sat
C 264	21	1.0	68661	3	AC024805	AC024805 Caenorhab	C 337	21	1.0	136693	9	HS164F3	HS164F3 Human DNA
C 265	21	1.0	69876	2	AC101484	AC101484 Mus muscu	C 338	21	1.0	138846	2	AC068478	AC068478 Homo sapi
C 266	21	1.0	72586	10	AL732542	AL732542 Mouse DNA	C 339	21	1.0	139121	8	AP004846	AP004846 Oryza sat
C 267	21	1.0	73516	2	AC100369	AC100369 Mus muscu	C 340	21	1.0	139505	2	AP004846	AP004846 Oryza sat
C 268	21	1.0	73516	2	AC100369	AC100369 Mus muscu	C 341	21	1.0	142414	8	AP004689	AP004689 Oryza sat
C 269	21	1.0	75342	3	CEV47H9C	CEV47H9C Pan trogl	C 342	21	1.0	142898	2	CR387993	CR387993 Danio rer
C 270	21	1.0	76213	2	AC108379	AC108379 Arabidops	C 343	21	1.0	143163	9	HSBK21C21	HSBK21C21 Human DNA
C 271	21	1.0	76336	8	AB077822	AB077822 Arabidops	C 344	21	1.0	143200	8	AP004380	AP004380 Oryza sat
C 272	21	1.0	77880	9	AC114766	AC114766 Homo sapi	C 345	21	1.0	144596	8	AP004574	AP004574 Oryza sat
C 273	21	1.0	78402	8	NCB16M17	NCB16M17 Neurospor	C 346	21	1.0	144596	8	AP004574	AP004574 Oryza sat
C 274	21	1.0	79318	3	AV17106582	AV17106582 Dictyoste	C 347	21	1.0	145146	2	AC126926	AC126926 Felis cat
C 275	21	1.0	80503	8	NC94C8	NC94C8 Neurospor	C 348	21	1.0	145975	2	AC126238	AC126238 Felis cat
C 276	21	1.0	81246	9	AB025629	AB025629 Arabidops	C 349	21	1.0	146207	2	AP004555	AP004555 Oryza sat
C 277	21	1.0	81677	8	AB025629	AB025629 Arabidops	C 350	21	1.0	146207	2	AP004555	AP004555 Oryza sat
C 278	21	1.0	81784	8	AC078893	AC078893 Oryza sat	C 351	21	1.0	146453	4	AY152827	AY152827 Danio rer
C 279	21	1.0	81996	10	BX470237	BX470237 Mouse DNA	C 352	21	1.0	146505	2	AC021604	AC021604 Homo sapi
C 280	21	1.0	83373	5	BX284635	BX284635 Zebrafish	C 353	21	1.0	146551	2	AC021604	AC021604 Homo sapi
C 281	21	1.0	84000	8	AC0010796	AC0010796 Arabidops	C 354	21	1.0	146570	3	AC117076	AC117076 Dictyoste
C 282	21	1.0	87885	8	AC007659	AC007659 Arabidops	C 355	21	1.0	146824	2	AC118745	AC118745 Mus muscu
C 283	21	1.0	88356	8	AB011479	AB011479 Arabidops	C 356	21	1.0	148232	2	CR848023	CR848023 Danio rer
C 284	21	1.0	89004	3	CEY69H2	CEY69H2 Caenorhab	C 357	21	1.0	148391	2	AC034174	AC034174 Homo sapi
C 285	21	1.0	89249	3	AC103567	AC103567 Caenorhab	C 358	21	1.0	149526	2	BX957346	BX957346 Danio rer
C 286	21	1.0	89479	8	AC006932	AC006932 Genomic s	C 359	21	1.0	150663	2	AC074258	AC074258 Trypanoso
C 287	21	1.0	95103	6	CQ754091	CQ754091 Sequence	C 360	21	1.0	151040	10	AC126040	AC126040 Mus muscu
C 288	21	1.0	96250	6	CQ754089	CQ754089 Sequence	C 361	21	1.0	151138	2	AC136727	AC136727 Mus muscu
C 289	21	1.0	97021	2	AC138255	AC138255 Mus muscu	C 362	21	1.0	151143	2	AC141740	AC141740 Apis mell
C 290	21	1.0	97789	8	AC004255	AC004255 Arabidops	C 363	21	1.0	151802	2	AC146431	AC146431 Pan trogl
C 291	21	1.0	97955	6	CQ754090	CQ754090 Sequence	C 364	21	1.0	152092	8	AP004363	AP004363 Oryza sat
C 292	21	1.0	99014	6	AX410782	AX410782 Sequence	C 365	21	1.0	154034	10	AL772336	AL772336 Mouse DNA
C 293	21	1.0	99014	9	HSU78027	HSU78027 Homo sapien	C 366	21	1.0	154216	2	AC120503	AC120503 Didelphis
C 294	21	1.0	99163	2	AL356436	AL356436 Homo sapi	C 367	21	1.0	154726	9	AL445923	AL445923 Human DNA
C 295	21	1.0	99659	10	AL732516	AL732516 Mouse DNA	C 368	21	1.0	155232	2	AC149215	AC149215 Mus muscu
C 296	21	1.0	101954	5	BX942844	BX942844 Zebrafish	C 369	21	1.0	155348	5	AL928820	AL928820 Zebrafish
C 297	21	1.0	103088	2	AC142395	AC142395 Medicago	C 370	21	1.0	156034	5	BX548043	BX548043 Zebrafish
C 298	21	1.0	103388	8	AC002294	AC002294 Arabidops	C 371	21	1.0	156419	8	AP002524	AP002524 Oryza sat
C 299	21	1.0	105726	10	AF037352	AF037352 Mus muscu	C 372	21	1.0	157348	2	AP002446	AP002446 Homo sapi
C 300	21	1.0	106159	4	AC124041	AC124041 Cryptocolag	C 373	21	1.0	159336	9	AC020584	AC020584 Homo sapi
C 301	21	1.0	106527	2	AC148396	AC148396 Medicago	C 374	21	1.0	159875	9	AC024023	AC024023 Homo sapi
C 302	21	1.0	106527	2	AC148396	AC148396 Medicago	C 375	21	1.0	160250	9	AC087173	AC087173 Homo sapi
C 303	21	1.0	106935	3	AC087079	AC087079 Caenorhab	C 376	21	1.0	160487	9	AC084058	AC084058 Homo sapi
C 304	21	1.0	107284	8	AP005290	AP005290 Oryza sat	C 377	21	1.0	162784	2	AC114632	AC114632 Homo sapi
C 305	21	1.0	108582	8	AC011663	AC011663 Arabidops	C 378	21	1.0	162911	9	AC073486	AC073486 Homo sapi
C 306	21	1.0	110000	2	AC105495	AC105495 Rattus no	C 379	21	1.0	163421	2	AL353792	AL353792 Homo sapi
C 307	21	1.0	110000	2	CEY19467	CEY19467 Continuation (2 of	C 380	21	1.0	163634	2	AC141374	AC141374 Rattus no
C 308	21	1.0	110000	2	CEY102G3	CEY102G3 Continuation (2 of	C 381	21	1.0	163980	2	CR847967	CR847967 Danio rer
C 309	21	1.0	110000	2	CEY113B8	CEY113B8 Continuation (2 of	C 382	21	1.0	164147	8	AP005784	AP005784 Oryza sat
C 310	21	1.0	110000	2	CEY113B8	CEY113B8 Continuation (3 of	C 383	21	1.0	165361	10	AC125109	AC125109 Mus muscu
C 311	21	1.0	110000	8	CR380952	CR380952 Continuation (9 of	C 384	21	1.0	165458	2	AC009795	AC009795 Homo sapi

531	21	1.0	263219	2	AC128778	AC128778 Rattus no	604	20	1.0	1645	6	AX509898	AX509898 Sequence
532	21	1.0	266344	9	AC005158	AC005158 Homo sapi	605	20	1.0	1666	5	CR761178	CR761178 Xenopus t
533	21	1.0	270693	2	AC097197	AC097197 Rattus no	606	20	1.0	1773	5	BC067243	BC067243 Homo sapi
534	21	1.0	278007	2	AC097197	AC097197 Rattus no	607	20	1.0	1789	5	XELXWNT	L07538 Frog wnt3A
535	21	1.0	278007	2	AC097197	AC097197 Rattus no	608	20	1.0	1836	4	AF219241	AF219241 Loxodonta
536	21	1.0	278377	2	AC129839	AC129839 Rattus no	609	20	1.0	1905	5	CR523409	CR523409 Gallus ga
537	21	1.0	280335	2	AC105705	AC105705 Rattus no	610	20	1.0	2000	6	AX508509	AX508509 Sequence
538	21	1.0	280417	2	AC095158	AC095158 Rattus no	611	20	1.0	2037	6	CQ782415	CQ782415 Sequence
539	21	1.0	290066	2	AC129421	AC129421 Rattus no	612	20	1.0	2037	6	BD127120	BD127120 Primer fo
540	21	1.0	299015	2	AC006842	AC006842 Caenorhab	613	20	1.0	2037	9	AK074489	AK074489 Homo sapi
541	21	1.0	299820	2	AC006842	AC006842 Caenorhab	614	20	1.0	2057	10	AF060178	AF060178 Mus muscu
542	21	1.0	299820	2	AC006842	AC006842 Caenorhab	615	20	1.0	2146	8	YSCPEP4	YSCPEP4 Saccharomy
543	21	1.0	300029	8	AE017105	AE017105 Oryza sat	616	20	1.0	2160	5	BC073416	BC073416 Xenopus l
544	21	1.0	300150	1	AP004594	AP004594 Cloanobac	617	20	1.0	2320	3	AK114986	AK114986 Ciona int
545	21	1.0	301450	1	AP003188	AP003188 Clostridi	618	20	1.0	2330	8	SCYPL154C	SCYPL154C S.cerevisia
546	21	1.0	302228	8	AE017070	AE017070 Oryza sat	619	20	1.0	2390	3	AK025438	AK025438 Homo sapi
547	21	1.0	304297	8	AE017088	AE017088 Oryza sat	620	20	1.0	2673	2	AC014043	AC014043 Drosophil
548	21	1.0	304297	8	AE017088	AE017088 Oryza sat	621	20	1.0	2680	3	AF065437	AF065437 Aedes alb
549	21	1.0	305962	2	AC006746	AC006746 Caenorhab	622	20	1.0	2695	8	AK118006	AK118006 Arabidops
550	21	1.0	305962	2	AC006746	AC006746 Caenorhab	623	20	1.0	2715	8	AK069180	AK069180 Oryza sat
551	21	1.0	333321	3	AC116986	AC116986 Dictyoate	624	20	1.0	2767	2	AC017589	AC017589 Drosophil
552	21	1.0	337720	2	AC121050	AC121050 Rattus no	625	20	1.0	2853	6	AX833477	AX833477 Sequence
553	21	1.0	348034	3	CR382400	CR382400 Plasmodi	626	20	1.0	2853	9	AK095249	AK095249 Homo sapi
554	21	1.0	349907	1	BX571874	BX571874 Photorhab	627	20	1.0	3007	9	BC034979	BC034979 Homo sapi
555	21	1.0	349980	6	CQ870290	CQ870290 Sequence	628	20	1.0	3008	9	BC028710	BC028710 Homo sapi
556	21	1.0	349980	6	AX344554	AX344554 Sequence	629	20	1.0	3028	9	BC030784	BC030784 Homo sapi
557	21	1.0	349980	6	AX344563	AX344563 Sequence	630	20	1.0	3073	9	HSM806062	HSM806062 BX537938 Homo sapi
558	21	1.0	349980	6	AX344563	AX344563 Sequence	631	20	1.0	3100	6	CQ850945	CQ850945 Sequence
559	21	1.0	349980	6	AX344563	AX344563 Sequence	632	20	1.0	3100	9	AK128147	AK128147 Homo sapi
560	21	1.0	349980	6	AX344563	AX344563 Sequence	633	20	1.0	3182	2	AC017715	AC017715 Drosophil
561	21	1.0	4240	6	AX245416	AX245416 Sequence	634	20	1.0	3230	6	CQ588287	CQ588287 Sequence
562	21	1.0	4240	6	AX245416	AX245416 Sequence	635	20	1.0	3266	9	HS20TOM5	HS20TOM5 AF126962 Homo sapi
563	21	1.0	425	6	AX533367	AX533367 Sequence	636	20	1.0	3471	1	STYHIN	STYHIN D13690 S.abortus-e
564	21	1.0	425	6	AX533367	AX533367 Sequence	637	20	1.0	3497	5	BC084216	BC084216 Xenopus l
565	21	1.0	425	6	AX533367	AX533367 Sequence	638	20	1.0	3775	8	AX072083	AX072083 Arabidops
566	21	1.0	425	6	AX533367	AX533367 Sequence	639	20	1.0	3853	3	CQ608645	CQ608645 Sequence
567	21	1.0	425	6	AX533367	AX533367 Sequence	640	20	1.0	4089	6	DMTNFB	DMTNFB V00246 Transposabl
568	21	1.0	425	6	AX533367	AX533367 Sequence	641	20	1.0	4096	8	SCYPL153C	SCYPL153C 273509 S.cerevisia
569	21	1.0	425	6	AX533367	AX533367 Sequence	642	20	1.0	4128	6	AX305892	AX305892 Sequence
570	21	1.0	425	6	AX533367	AX533367 Sequence	643	20	1.0	4128	10	MUSFTSP12A	MUSFTSP12A M70641 Mouse Fisp-
571	21	1.0	425	6	AX533367	AX533367 Sequence	644	20	1.0	4172	6	AX345616	AX345616 Sequence
572	21	1.0	425	6	AX533367	AX533367 Sequence	645	20	1.0	4743	9	HUM19DC93Z	HUM19DC93Z L78750 Homo sapien
573	21	1.0	425	6	AX533367	AX533367 Sequence	646	20	1.0	4781	10	AY591641	AY591641 Mus muscu
574	21	1.0	425	6	AX533367	AX533367 Sequence	647	20	1.0	5158	6	AX300905	AX300905 Sequence
575	21	1.0	425	6	AX533367	AX533367 Sequence	648	20	1.0	5345	2	AC014042	AC014042 Drosophil
576	21	1.0	425	6	AX533367	AX533367 Sequence	649	20	1.0	5351	6	AX251238	AX251238 Sequence
577	21	1.0	425	6	AX533367	AX533367 Sequence	650	20	1.0	5571	6	AX251941	AX251941 Sequence
578	21	1.0	425	6	AX533367	AX533367 Sequence	651	20	1.0	5571	6	AX344343	AX344343 Sequence
579	21	1.0	425	6	AX533367	AX533367 Sequence	652	20	1.0	5571	6	AX348740	AX348740 Sequence
580	21	1.0	425	6	AX533367	AX533367 Sequence	653	20	1.0	5608	9	HSM809103	HSM809103 AX323784 Homo sapi
581	21	1.0	425	6	AX533367	AX533367 Sequence	654	20	1.0	5986	6	AX323784	AX323784 Sequence
582	21	1.0	425	6	AX533367	AX533367 Sequence	655	20	1.0	6081	8	AF096095	AF096095 Arabidops
583	21	1.0	425	6	AX533367	AX533367 Sequence	656	20	1.0	6458	6	BD223811	BD223811 Novel met
584	21	1.0	425	6	AX533367	AX533367 Sequence	657	20	1.0	6656	6	AX453099	AX453099 Sequence
585	21	1.0	425	6	AX533367	AX533367 Sequence	658	20	1.0	6656	6	AX281211	AX281211 Sequence
586	21	1.0	425	6	AX533367	AX533367 Sequence	659	20	1.0	6656	6	AX281211	AX281211 Sequence
587	21	1.0	425	6	AX533367	AX533367 Sequence	660	20	1.0	6795	9	AB014605	AB014605 Homo sapi
588	21	1.0	425	6	AX533367	AX533367 Sequence	661	20	1.0	6876	6	AX346666	AX346666 Sequence
589	21	1.0	425	6	AX533367	AX533367 Sequence	662	20	1.0	8029	1	ECFAPGK	ECFAPGK X14436 Escherichia
590	21	1.0	425	6	AX533367	AX533367 Sequence	663	20	1.0	8029	14	AY395706	AY395706 Human pap
591	21	1.0	425	6	AX533367	AX533367 Sequence	664	20	1.0	8092	2	AX281525	AX281525 Sequence
592	21	1.0	425	6	AX533367	AX533367 Sequence	665	20	1.0	8662	6	AX281525	AX281525 Sequence
593	21	1.0	425	6	AX533367	AX533367 Sequence	666	20	1.0	10105	2	AC017666	AC017666 Drosophil
594	21	1.0	425	6	AX533367	AX533367 Sequence	667	20	1.0	10120	1	TMRPO	TMRPO X72695 T.maritima
595	21	1.0	425	6	AX533367	AX533367 Sequence	668	20	1.0	10425	3	CQ607523	CQ607523 Sequence
596	21	1.0	425	6	AX533367	AX533367 Sequence	669	20	1.0	10762	3	AC119287	AC119287 Caenorhab
597	21	1.0	425	6	AX533367	AX533367 Sequence	670	20	1.0	10891	6	AX345366	AX345366 Sequence
598	21	1.0	425	6	AX533367	AX533367 Sequence	671	20	1.0	11293	1	AE005523	AE005523 Escherich
599	21	1.0	425	6	AX533367	AX533367 Sequence	672	20	1.0	11490	1	AE015305	AE015305 Shigella
600	21	1.0	425	6	AX533367	AX533367 Sequence	673	20	1.0	12511	1	AE002129	AE002129 Ureaplaem
601	21	1.0	425	6	AX533367	AX533367 Sequence	674	20	1.0	12610	6	CQ806991	CQ806991 Sequence
602	21	1.0	425	6	AX533367	AX533367 Sequence	675	20	1.0	14687	3	U80841	U80841 Caenorhabd
603	21	1.0	425	6	AX533367	AX533367 Sequence	676	20	1.0	15399	6	AX346416	AX346416 Sequence

531	21	1.0	263219	2	AC128778	AC128778 Rattus no
532	21	1.0	266344	9	AC005158	AC005158 Homo sapi
533	21	1.0	270693	2	AC097197	AC097197 Rattus no
534	21	1.0	270893	2	AC097197	AC097197 Rattus no
535	21	1.0	278007	2	AC006799	AC006799 Caenorhab
536	21	1.0	278377	2	AC129839	AC129839 Rattus no
537	21	1.0	280335	2	AC105705	AC105705 Rattus no
538	21	1.0	280417	2	AC095158	AC095158 Rattus no
539	21	1.0	290066	2	AC129421	AC129421 Rattus no
540	21	1.0	299015	2	AC006842	AC006842 Caenorhab
541	21	1.0	299820	2	AC006803	AC006803 Caenorhab
542	21	1.0	299820	2	AC006871	AC006871 Caenorhab
543	21	1.0	300029	8	AE017105	AE017105 Oryza sat
544	21	1.0	300150	1	AP004594	AP004594 Oceanobac
545	21	1.0	301450	1	AP003188	AP003188 Clostridi
546	21	1.0	302228	8	AE017070	AE017070 Oryza sat
547	21	1.0	304297	8	AE017088	AE017088 Oryza sat
548	21	1.0	305962	2	AC006746	AC006746 Caenorhab
549	21	1.0	305962	2	AC006746	AC006746 Caenorhab
550	21	1.0	333321	3	AC116986	AC116986 Dictyoste
551	21	1.0	337720	2	AC121050	AC121050 Rattus no
552	21	1.0	348034	3	CR382400	CR382400 Plasmodi
553	21	1.0	349907	1	BX571874	BX571874 Photorhab
554	21	1.0	349980	6	CQ870290	CQ870290 Sequence
555	21	1.0	349980	6	AX344554	AX344554 Sequence
556	21	1.0	349980	6	AX344563	AX344563 Sequence
557	21	1.0	349980	6	AX344563	AX344563 Sequence
558	21	1.0	349980	6	AX360398	AX360398 Sequence
559	21	1.0	349980	6	AX360425	AX360425 Sequence
560	21	1.0	349980	6	AX441509	AX441509 Sequence
561	21	1.0	349980	6	AX441509	AX441509 Sequence
562	21	1.0	349980	6	AX441509	AX441509 Sequence
563	21	1.0	349980	6	AX441509	AX441509 Sequence
564	21	1.0	349980	6	AX441509	AX441509 Sequence
565	21	1.0	349980	6	AX441509	AX441509 Sequence
566	21	1.0	349980	6	AX441509	AX441509 Sequence
567	21	1.0	349980	6	AX441509	AX441509 Sequence
568	21	1.0	349980	6	AX441509	AX441509 Sequence
569	21	1.0	349980	6	AX441509	AX441509 Sequence
570	21	1.0	349980	6	AX441509	AX441509 Sequence
571	21	1.0	349980	6	AX441509	AX441509 Sequence
572	21	1.0	349980	6	AX441509	AX441509 Sequence
573	21	1.0	349980	6	AX441509	AX441509 Sequence
574	21	1.0	349980	6	AX441509	AX441509 Sequence
575	21	1.0	349980	6	AX441509	AX441509 Sequence
576	21	1.0	349980	6	AX441509	AX441509 Sequence
577	21	1.0	349980	6	AX441509	AX441509 Sequence
578	21	1.0	349980	6	AX441509	AX441509 Sequence
579	21	1.0	349980	6	AX441509	AX441509 Sequence
580	21	1.0	349980	6	AX441509	AX441509 Sequence
581	21	1.0	349980	6	AX441509	AX441509 Sequence
582	21	1.0	349980	6	AX441509	AX441509 Sequence
583	21	1.0	349980	6	AX441509	AX441509 Sequence
584	21	1.0	349980	6	AX441509	AX441509 Sequence
585	21	1.0	349980	6	AX441509	AX441509 Sequence
586	21	1.0	349980	6	AX441509	AX441509 Sequence
587	21	1.0	349980	6	AX441509	AX441509 Sequence
588	21	1.0	349980	6	AX441509	AX441509 Sequence
589	21	1.0	349980	6	AX441509	AX441509 Sequence
590	21	1.0	349980	6	AX441509	AX441509 Sequence
591	21	1.0	349980	6	AX441509	AX441509 Sequence
592	21	1.0	349980	6	AX441509	AX441509 Sequence
593	21	1.0	349980	6	AX441509	AX441509 Sequence
594	21	1.0	349980	6	AX441509	AX441509 Sequence
595	21	1.0	349980	6	AX441509	AX441509 Sequence
596	21	1.0	349980	6	AX441509	AX441509 Sequence
597	21	1.0	349980	6	AX441509	AX441509 Sequence
598	21	1.0	349980	6	AX441509	AX441509 Sequence
599	21	1.0	349980	6	AX441509	AX441509 Sequence
600	21	1.0	349980	6	AX441509	AX441509 Sequence
601	21	1.0	349980	6	AX441509	AX441509 Sequence
602	21	1.0	349980	6	AX441509	AX441509 Sequence
603	21	1.0	349980	6	AX441509	AX441509 Sequence

c 677	20	1.0	16918	6	AX346519	Sequence	AX346519	c 750	20	1.0	66253	2	AC023372	2	AC023372	Homo sapi
c 678	20	1.0	20420	1	AE001724	Thermotog	AE001724	c 751	20	1.0	66796	2	AC017435	2	AC017435	Drosophil
c 679	20	1.0	20513	1	AE008826	Salmonell	AE008826	c 752	20	1.0	67552	8	AP006677	8	AP006677	Lotus cor
c 680	20	1.0	21123	2	AC012820	Drosophil	AC012820	c 753	20	1.0	67706	9	AC073517	9	AC073517	Homo sapi
c 681	20	1.0	21520	3	AC024813	Caenorhab	AC024813	c 754	20	1.0	67970	3	PFMAL1P3	3	PFMAL1P3	Plasmodiu
c 682	20	1.0	22660	6	C0584033	Sequence	C0584033	c 755	20	1.0	68301	9	AL158065	9	AL158065	Human DNA
c 683	20	1.0	23058	3	AF099927	Caenorhab	AF099927	c 756	20	1.0	69381	9	HSJ301L19	9	HSJ301L19	Human DNA
c 684	20	1.0	23764	3	AC006723	Caenorhab	AC006723	c 757	20	1.0	69692	8	AC121763	8	AC121763	Genomic B
c 685	20	1.0	24686	3	CEY43F11A	Caenorhab	CEY43F11A	c 758	20	1.0	70145	2	AC101291	2	AC101291	Mus muscu
c 686	20	1.0	25426	3	AC006747	Caenorhab	AC006747	c 759	20	1.0	70704	8	NCB8L21	8	NCB8L21	Neurospor
c 687	20	1.0	25568	3	AC116955	Dictyoste	AC116955	c 760	20	1.0	72175	2	AC101418	2	AC101418	Mus muscu
c 688	20	1.0	25851	3	AF025466	Caenorhab	AF025466	c 761	20	1.0	72175	2	AC101418	2	AC101418	Mus muscu
c 689	20	1.0	26547	3	U70844	Caenorhabd	U70844	c 762	20	1.0	72412	2	AC101594	2	AC101594	Mus muscu
c 690	20	1.0	26874	3	CEB10255	Caenorhabd	CEB10255	c 763	20	1.0	72412	2	AC101594	2	AC101594	Mus muscu
c 691	20	1.0	29546	3	AF003390	Caenorhab	AF003390	c 764	20	1.0	73101	8	AP006122	8	AP006122	Lotus cor
c 692	20	1.0	29976	3	U50197	Caenorhabd	U50197	c 765	20	1.0	75073	3	CEY48A6B	3	CEY48A6B	Caenorhab
c 693	20	1.0	30305	3	AF100305	Caenorhab	AF100305	c 766	20	1.0	75289	8	AB023046	8	AB023046	Arabidops
c 694	20	1.0	31876	3	AF078783	Caenorhab	AF078783	c 767	20	1.0	78172	8	AB010070	8	AB010070	Arabidops
c 695	20	1.0	32323	2	AC022228	Mus muscu	AC022228	c 768	20	1.0	82033	8	AB011476	8	AB011476	Arabidops
c 696	20	1.0	32940	3	AF022972	Caenorhab	AF022972	c 769	20	1.0	83024	9	AC000389	9	AC000389	Genomic B
c 697	20	1.0	33000	3	CEK11H3	Caenorhabd	CEK11H3	c 770	20	1.0	83601	9	AC079172	9	AC079172	Homo sapi
c 698	20	1.0	33796	3	U56964	Caenorhabd	U56964	c 771	20	1.0	85214	8	AC005396	8	AC005396	Arabidops
c 699	20	1.0	35121	2	CEC43A10	Caenorhabd	CEC43A10	c 772	20	1.0	85812	2	AC040952	2	AC040952	Homo sapi
c 700	20	1.0	35137	8	AC007196	Arabidops	AC007196	c 773	20	1.0	88839	3	AC084447	3	AC084447	Caenorhab
c 701	20	1.0	36096	6	AX059472	Sequence	AX059472	c 774	20	1.0	89840	8	AC004705	8	AC004705	Arabidops
c 702	20	1.0	36494	3	CEP59D12	Caenorhabd	CEP59D12	c 775	20	1.0	90335	8	ATT5N23	8	ATT5N23	Genomic B
c 703	20	1.0	36582	3	AF036689	Caenorhab	AF036689	c 776	20	1.0	90901	9	HSJ417120	9	HSJ417120	Homo sapi
c 704	20	1.0	36888	3	U29378	Caenorhabd	U29378	c 777	20	1.0	90963	2	AC079626	2	AC079626	Mus muscu
c 705	20	1.0	37034	3	CBRGA7D14	Caenorhabd	CBRGA7D14	c 778	20	1.0	91714	8	ATAC001645	8	ATAC001645	Arabidops
c 706	20	1.0	37059	3	CEK02E2	Caenorhabd	CEK02E2	c 779	20	1.0	91755	8	AC142210	8	AC142210	Solanum d
c 707	20	1.0	37521	2	CE149354	Phakopsor	CE149354	c 780	20	1.0	91947	5	BX324211	5	BX324211	Zebrafish
c 708	20	1.0	38856	3	CFY43P8A	Caenorhab	CFY43P8A	c 781	20	1.0	93217	2	AC023171	2	AC023171	Homo sapi
c 709	20	1.0	39121	3	CBF09C6	Caenorhabd	CBF09C6	c 782	20	1.0	93342	9	AC087245	9	AC087245	Homo sapi
c 710	20	1.0	39236	3	CEFS9A1	Caenorhabd	CEFS9A1	c 783	20	1.0	93451	2	AC130446	2	AC130446	Continuation (4 of
c 711	20	1.0	39271	3	CEFS52C2	Caenorhabd	CEFS52C2	c 784	20	1.0	94088	5	BX323553	5	BX323553	Zebrafish
c 712	20	1.0	39348	9	AL354670	Human DNA	AL354670	c 785	20	1.0	95765	8	AC006528	8	AC006528	Arabidops
c 713	20	1.0	39555	3	CEZK262	Caenorhabd	CEZK262	c 786	20	1.0	96880	5	AC107364	5	AC107364	Danio rer
c 714	20	1.0	39634	2	AC145715	Homo sapi	AC145715	c 787	20	1.0	97006	8	ATF16G20	8	ATF16G20	Arabidops
c 715	20	1.0	39974	3	AF099921	Caenorhab	AF099921	c 788	20	1.0	100000	9	AB020861	9	AB020861	Homo sapi
c 716	20	1.0	40466	3	U58749	Caenorhabd	U58749	c 789	20	1.0	101295	3	CEY48B6A	3	CEY48B6A	Caenorhab
c 717	20	1.0	40766	3	AF101305	Caenorhab	AF101305	c 790	20	1.0	101647	8	AC004665	8	AC004665	Arabidops
c 718	20	1.0	41627	3	U41528	Caenorhabd	U41528	c 791	20	1.0	101679	3	CEY43F8B	3	CEY43F8B	Caenorhab
c 719	20	1.0	41708	3	AF036700	Caenorhab	AF036700	c 792	20	1.0	102495	3	CEY80D3A	3	CEY80D3A	Caenorhab
c 720	20	1.0	42703	3	CEC09F9	Caenorhab	CEC09F9	c 793	20	1.0	102574	2	AC017935	2	AC017935	Drosophil
c 721	20	1.0	42886	9	AC016762	Homo sapi	AC016762	c 794	20	1.0	102700	2	BX248101	2	BX248101	Continuation (5 of
c 722	20	1.0	43884	3	CEC25F9	Caenorhabd	CEC25F9	c 795	20	1.0	103632	8	AF074021	8	AF074021	Arabidops
c 723	20	1.0	45232	3	AF100657	Caenorhab	AF100657	c 796	20	1.0	103931	8	AC020646	8	AC020646	Genomic B
c 724	20	1.0	45510	3	CEC32A3	Caenorhab	CEC32A3	c 797	20	1.0	104749	9	AL772370	9	AL772370	Human DNA
c 725	20	1.0	45635	3	AF026205	Caenorhab	AF026205	c 798	20	1.0	104798	3	AC140918	3	AC140918	Caenorhab
c 726	20	1.0	46387	2	U82212	Homo sapien	U82212	c 799	20	1.0	106632	8	AP004500	8	AP004500	Lotus cor
c 727	20	1.0	47328	6	AX059532	Sequence	AX059532	c 800	20	1.0	106883	5	AL928842	5	AL928842	Zebrafish
c 728	20	1.0	47440	9	U73509	Homo sapien	U73509	c 801	20	1.0	106898	2	AC147903	2	AC147903	Xenopus t
c 729	20	1.0	48397	2	AC015399	Drosophil	AC015399	c 802	20	1.0	106949	3	CEY52B11A	3	CEY52B11A	Caenorhab
c 730	20	1.0	51015	9	AL732292	Human DNA	AL732292	c 803	20	1.0	107271	8	ATT8M16	8	ATT8M16	Arabidops
c 731	20	1.0	52139	3	AC006790	Caenorhab	AC006790	c 804	20	1.0	107995	2	HSJ356J11	2	HSJ356J11	Homo sapi
c 732	20	1.0	52684	2	AC014796	Caenorhab	AC014796	c 805	20	1.0	108287	2	AP003814	2	AP003814	Oryza sat
c 733	20	1.0	54475	3	AC024812	Caenorhab	AC024812	c 806	20	1.0	108459	3	ATT22A6	3	ATT22A6	Arabidops
c 734	20	1.0	55786	8	SLACHXVI	X96770 S.cerevisia	X96770 S.cerevisia	c 807	20	1.0	109299	8	AC117838	8	AC117838	Caenorhab
c 735	20	1.0	55965	9	AC104653	Homo sapi	AC104653	c 808	20	1.0	109672	8	AP004119	8	AP004119	Oryza sat
c 736	20	1.0	56012	9	AC100094	Mus muscu	AC100094	c 809	20	1.0	109918	9	AC016546	9	AC016546	Homo sapi
c 737	20	1.0	57795	9	AC004219	Homo sapi	AC004219	c 810	20	1.0	110000	1	U00096_30	1	U00096_30	Continuation (31 o
c 738	20	1.0	58220	2	AC091188	Homo sapi	AC091188	c 811	20	1.0	110000	1	AE017225	1	AE017225	Continuation (3 of
c 739	20	1.0	58804	8	CR380949	Continuation (6 of	Continuation (6 of	c 812	20	1.0	110000	1	AE017261	1	AE017261	Continuation (6 of
c 740	20	1.0	59533	3	AC084450	Caenorhab	AC084450	c 813	20	1.0	110000	1	AE017308	1	AE017308	Continuation (2 of
c 741	20	1.0	59577	9	AL589796	Human DNA	AL589796	c 814	20	1.0	110000	1	AE017334	1	AE017334	Continuation (3 of
c 742	20	1.0	61910	2	AC101194	Mus muscu	AC101194	c 815	20	1.0	110000	2	AE017355	2	AE017355	Continuation (3 of
c 743	20	1.0	63680	2	AC101117	Mus muscu	AC101117	c 816	20	1.0	110000	1	CP000001	1	CP000001	Continuation (3 of
c 744	20	1.0	63747	3	AC025727	Caenorhab	AC025727	c 817	20	1.0	110000	2	AC010714	2	AC010714	Continuation (3 of
c 745	20	1.0	63747	3	AC025727	Caenorhab	AC025727	c 818	20	1.0	110000	2	AC099211	2	AC099211	Continuation (3 of
c 746	20	1.0	64093	3	AC124291	Homo sapi	AC124291	c 819	20	1.0	110000	2	AC117865	2	AC117865	Continuation (3 of
c 747	20	1.0	64136	8	AB024031	Arabidops	AB024031	c 820	20	1.0	110000	2	AC120739	2	AC120739	Rattus no
c 748	20	1.0	64670	2	AC136714	Continuation (4 of	Continuation (4 of	c 821	20	1.0	110000	2	AC120739	2	AC120739	Continuation (2 of
c 749	20	1.0	66253	2	AC023372	Homo sapi	AC023372	c 822	20	1.0	110000	2	AC127447	2	AC127447	Continuation (3 of

c 823	20	1.0 110000	2	BX119990.2	Continuation (3 of	896	20	1.0 138102	9	AC004866	AC004866 Homo sapi
c 824	20	1.0 110000	2	CVY102G3.2	Continuation (3 of	c 897	20	1.0 138303	8	AC137077	AC137077 Medicago
c 825	20	1.0 110000	2	CR38160.1	Continuation (2 of	c 898	20	1.0 139549	7	AC114644	AC114644 Mus muscu
c 826	20	1.0 110000	2	CR759862.2	Continuation (3 of	c 899	20	1.0 139715	8	CR848037	CR848037 Danio rer
c 827	20	1.0 110000	2	PFMAL7P1.09	Continuation (10 o	c 900	20	1.0 139969	8	AC130811	AC130811 Medicago
c 828	20	1.0 110000	2	PFMAL8P1.01	Continuation (2 of	c 901	20	1.0 140261	10	AC109660	AC109660 Rattus no
c 829	20	1.0 110000	3	AC116984.3	Continuation (4 of	c 902	20	1.0 140593	8	AP004797	AP004797 Oryza sat
c 830	20	1.0 110000	3	AS003426.1	Continuation (2 of	c 903	20	1.0 140615	2	AP000726	AP000726 Homo sapi
c 831	20	1.0 110000	3	AS003426.1	Continuation (2 of	c 904	20	1.0 140954	2	AC141538	AC141538 Rattus no
c 832	20	1.0 110000	8	CR382124.15	Continuation (16 o	c 905	20	1.0 141258	2	AC141674	AC141674 Apis mell
c 833	20	1.0 110000	8	CR382132.30	Continuation (31 o	c 906	20	1.0 141345	2	AC151422	AC151422 Bos tauru
c 834	20	1.0 110000	8	CR382132.30	Continuation (32 o	c 907	20	1.0 141744	1	ECU28377	ECU28377 Escherichia
c 835	20	1.0 110000	3	AY043292.31	Continuation (32 o	c 908	20	1.0 142068	8	AP003723	AP003723 Oryza sat
c 836	20	1.0 110623	3	AY043292.31	Continuation (32 o	c 909	20	1.0 142562	9	AL662852	AL662852 Human DNA
c 837	20	1.0 110893	8	FSF19	Continuation (31 o	c 910	20	1.0 142649	10	AC134847	AC134847 Mus muscu
c 838	20	1.0 110960	3	CR393A1A	Continuation (31 o	c 911	20	1.0 143113	8	AP000559	AP000559 Oryza sat
c 839	20	1.0 111253	9	HS273F20	Continuation (31 o	c 912	20	1.0 143369	9	AC006316	AC006316 Homo sapi
c 840	20	1.0 111714	2	AL359432	Continuation (31 o	c 913	20	1.0 143459	2	AC136088	AC136088 Rattus no
c 841	20	1.0 112085	9	AL133544	Continuation (31 o	c 914	20	1.0 143499	2	AC141969	AC141969 Rattus no
c 842	20	1.0 112369	2	AC005861	Continuation (31 o	c 915	20	1.0 143913	2	AC124827	AC124827 Mus muscu
c 843	20	1.0 112495	2	AL691460	Continuation (31 o	c 916	20	1.0 144511	2	AX927332	AX927332 Danio rer
c 844	20	1.0 112978	9	AC022139	Continuation (31 o	c 917	20	1.0 144563	8	CNS08C7P	CNS08C7P Human DNA
c 845	20	1.0 113045	2	AP000707	Continuation (31 o	c 918	20	1.0 144648	9	AL391832	AL391832 Human DNA
c 846	20	1.0 113539	9	AL353681	Continuation (31 o	c 919	20	1.0 144868	2	AC079508	AC079508 Mus muscu
c 847	20	1.0 114031	8	AC139354	Continuation (31 o	c 920	20	1.0 144969	8	AC137547	AC137547 Oryza sat
c 848	20	1.0 114972	9	AC016547	Continuation (31 o	c 921	20	1.0 145137	2	AC147495	AC147495 Bos tauru
c 849	20	1.0 115270	8	AC016517	Continuation (31 o	c 922	20	1.0 145137	8	AP005301	AP005301 Oryza sat
c 850	20	1.0 115289	8	AC150244	Continuation (31 o	c 923	20	1.0 145625	2	AC131010	AC131010 Homo sapi
c 851	20	1.0 115507	9	AC083950	Continuation (31 o	c 924	20	1.0 145634	10	AC127555	AC127555 Mus muscu
c 852	20	1.0 115963	8	F28J9	Continuation (31 o	c 925	20	1.0 145658	9	AC093154	AC093154 Homo sapi
c 853	20	1.0 116252	9	AL445228	Continuation (31 o	c 926	20	1.0 145937	2	AL355600	AL355600 Homo sapi
c 854	20	1.0 117372	9	AC010374	Continuation (31 o	c 927	20	1.0 146343	10	AC137147	AC137147 Mus muscu
c 855	20	1.0 117771	9	AC112906	Continuation (31 o	c 928	20	1.0 146454	14	AF410153	AF410153 Swinepox
c 856	20	1.0 118172	9	AC005912	Continuation (31 o	c 929	20	1.0 146963	10	AC101811	AC101811 Mus muscu
c 857	20	1.0 118196	8	AC005824	Continuation (31 o	c 930	20	1.0 147111	8	OSJN00179	OSJN00179 Oryza sat
c 858	20	1.0 118429	2	AL158017	Continuation (31 o	c 931	20	1.0 147156	2	AC025742	AC025742 Homo sapi
c 859	20	1.0 118468	2	AP005549	Continuation (31 o	c 932	20	1.0 147442	2	CR383683	CR383683 Danio rer
c 860	20	1.0 118533	9	AC008436	Continuation (31 o	c 933	20	1.0 147452	8	AC026815	AC026815 Oryza sat
c 861	20	1.0 120548	3	AC024798	Continuation (31 o	c 934	20	1.0 147664	4	AC144403	AC144403 Felis cat
c 862	20	1.0 120836	9	AC097457	Continuation (31 o	c 935	20	1.0 147836	8	AP003983	AP003983 Oryza sat
c 863	20	1.0 121377	6	CQ870474	Continuation (31 o	c 936	20	1.0 148496	2	AC134956	AC134956 Tetraodon
c 864	20	1.0 121448	9	AC010738	Continuation (31 o	c 937	20	1.0 148848	8	AP005426	AP005426 Oryza sat
c 865	20	1.0 121922	2	AP000576	Continuation (31 o	c 938	20	1.0 149052	2	AC130409	AC130409 Homo sapi
c 866	20	1.0 122151	8	NCB23420	Continuation (31 o	c 939	20	1.0 149109	2	AC101018	AC101018 Rattus no
c 867	20	1.0 122972	2	AL691434	Continuation (31 o	c 940	20	1.0 149369	10	AL607123	AL607123 Mouse DNA
c 868	20	1.0 123042	10	AC133583	Continuation (31 o	c 941	20	1.0 149502	10	AC130721	AC130721 Mus muscu
c 869	20	1.0 124254	10	AF450245	Continuation (31 o	c 942	20	1.0 150348	2	AC127477	AC127477 Felis cat
c 870	20	1.0 125290	9	AC004986	Continuation (31 o	c 943	20	1.0 150446	2	AC118530	AC118530 Rattus no
c 871	20	1.0 125632	8	AC015446	Continuation (31 o	c 944	20	1.0 150578	2	AC135551	AC135551 Sus scrof
c 872	20	1.0 126191	8	AC148815	Continuation (31 o	c 945	20	1.0 150655	9	AC025887	AC025887 Homo sapi
c 873	20	1.0 126356	2	AC006876	Continuation (31 o	c 946	20	1.0 150673	2	AC134704	AC134704 Rattus no
c 874	20	1.0 126891	2	AC105257	Continuation (31 o	c 947	20	1.0 151017	9	AL591431	AL591431 Human DNA
c 875	20	1.0 128418	8	AC135793	Continuation (31 o	c 948	20	1.0 151027	2	AC019003	AC019003 Homo sapi
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c 877	20	1.0 129782	5	BX120005	Continuation (31 o	c 950	20	1.0 151367	2	AC141764	AC141764 Apis mell
c 878	20	1.0 129808	9	AC079760	Continuation (31 o	c 951	20	1.0 151752	2	AC010779	AC010779 Homo sapi
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c 880	20	1.0 130699	2	AC137081	Continuation (31 o	c 953	20	1.0 151945	2	AC137701	AC137701 Medicago
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c 894	20	1.0 137202	2	AC138599	Continuation (31 o	c 967	20	1.0 153454	2	CR356234	CR356234 Danio rer
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ALIGNMENTS

RESULT 1
AX548023 2030 bp DNA linear PAT 26-NOV-2002
LOCUS Sequence 1 from Patent WO02068665.
DEFINITION AX548023
ACCESSION AX548023
VERSION AX548023.1 GI:25813131
KEYWORDS
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids.II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Thomas, T., Nuccio, M. and Hsieh, T.F.
TITLE Constitutive promoter from arabidopsis
JOURNAL Patent: WO 02068665-A 1 06-SEP-2002;
Rbioio (PR)
FEATURES
source Location/Qualifiers
1..2030
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 2030; DB 6; Length 2030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1381	TACTAGGGTTGTCATATTTTTCCGAGAAATATACAGAGGAACAAAGTTAGTGATATAT	1440
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RESULT 2			
AX548024			
LOCUS			
Sequence 2 from Patent WO02068665.			
AX548024			
ACCESSION			
AX548024.1			
VERSION			
GI:25813132			
KEYWORDS			
SOURCE			
ORGANISM			
Arabidopsis thaliana (thale cress)			
Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
1			
REFERENCE			
AUTHORS			
Thomas, T., Nuccio, M. and Heieh, T.F.			
TITLE			
Constitutive promoter from arabidopsis			
JOURNAL			
Patent: WO 02068665-A 2 06-SEP-2002;			
Rbioio (FR)			

FEATURES		Location/Qualifiers	
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		Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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RESULT 3

ATF1C12

LOCUS

DEFINITION

Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSA

project).

ACCESSION

AL022224

VERSION

AL022224.1

GI:3059018

KEYWORDS

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1

Bevan,M., Terry,N., Ardiles,W., Buyssehaert,C., Dasseville,R., De

Clerck,R., De Keyser,A., Neyt,P., Rouze,P., Van Den Daele,H.,

Villarroel,R., Gielens,J., Van Montagu,M., Bancroft,I., Mewes,H.W.,

Mayer,K.F.X., Lemcke,K. and Schueller,C.

Unpublished

2 (bases 1 to 111945)

EU Arabidopsis sequencing, project.

Direct Submission

Submitted (30-SEP-1999) MIPS, at the Max-Planck-Institut fuer

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schueller@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

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On Apr 18, 1998 this sequence version replaced gi:2982425.

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

Location/Qualifiers

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REFERENCE

AUTHORS

JOURNAL

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

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RESULT 4

ATCHRIV52

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

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Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52.

AL161552

GI:7268789

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 82704)

Murphy, G., Ridley, P., Hudson, S., Mewes, H.W., Lemcke, K. and

Mayer, K.F.X.

Unpublished

2 (bases 67424 to 179368)

Terry, N., Ardles, W., Buysshaert, C., Daseville, R., De Clerck, R.,

De Keyser, A., Neyt, P., Rouze, P., Van Den Daele, H., Villaroel, R.,

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VERSION			
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REFERENCE			
AUTHORS		Harper, J.F., Kreps, J., Wang, X. and Zhu, T.	
TITLE		Stress-regulated genes of plants, transgenic plants containing	
		same, and methods of use	
JOURNAL		Patent: WO 0216655-A 4152 28-FEB-2002;	
		The Scripps Research Institute (US); Syngenta Participations AG	
		(CH)	
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AX507890/c		288 bp	DNA
LOCUS	AX507890	Arabidopsis thaliana transposon insertion STS SM_3.4802, sequence	linear STS 11-JUN-2003
DEFINITION	AX507890	tagged site.	
ACCESSION	AX507890		
VERSION	AX507890.1	GI:21690190	
KEYWORDS		STS; STS, sequence tagged site.	
SOURCE		Arabidopsis thaliana (thale cress)	
ORGANISM		Arabidopsis thaliana	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M. Unpublished

2 (bases 1 to 288)

Clarke, J.H.
Direct Submission
Submitted (02-JUL-2002) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon B5SRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N10915.

FEATURES
Location/Qualifiers
source
1..288
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AL022224"
/notes="Derived from superpool NASC code Unknown"
STs
1..288
/standard_name="SM_3.4802"

ORIGIN
Query Match 10.3%; Score 209; DB 11; Length 288;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1167 TAAATTCAGAGACAAATTAATCAGTTCGTGCTGTTGGAGAGAGAACAGATCAA 1226
Db 209 TAAATTCAGAGACAAATTAATCAGTTCGTGCTGTTGGAGAGAGAACAGATCAA 150

Qy 1227 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAATCT 1286
Db 149 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAATCT 90

Qy 1287 TAAATTAACAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 1346
Db 89 TAAATTAACAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 30

Qy 1347 TTTTAGTTCATGTAATGAATCTGTTTT 1375
Db 29 TTTTAGTTCATGTAATGAATCTGTTTT 1

RESULT 7
BX295033/c
LOCUS
DEFINITION
Arabidopsis thaliana transposon insertion STS SM_3.33484, sequence tagged site.
ACCESSION
BX295033
VERSION
BX295033.1 GI:29149723
KEYWORDS
STS; STS, sequence tagged site.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M. Unpublished

2 (bases 1 to 290)

Clarke, J.H.
Direct Submission
Submitted (20-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon B5SRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N120195.

FEATURES
Location/Qualifiers
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/notes="Derived from superpool 1.28 NASC code N40027"
STs
1..290
/standard_name="SM_3.33484"

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Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1167 TAAATTCAGAGACAAATTAATCAGTTCGTGCTGTTGGAGAGAGAACAGATCAA 1226
Db 209 TAAATTCAGAGACAAATTAATCAGTTCGTGCTGTTGGAGAGAGAACAGATCAA 150

Qy 1227 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAATCT 1286
Db 149 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAATCT 90

Qy 1287 TAAATTAACAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 1346
Db 89 TAAATTAACAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 30

Qy 1347 TTTTAGTTCATGTAATGAATCTGTTTT 1375
Db 29 TTTTAGTTCATGTAATGAATCTGTTTT 1

RESULT 8
AY086004
LOCUS
DEFINITION
Arabidopsis thaliana clone 20592 mRNA, complete sequence.
ACCESSION
AY086004
VERSION
AY086004.1 GI:21404714
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)

2008475
MEDLINE
12093376
PUBMED
2 (bases 1 to 1001)
Brower, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

Full-length cDNA from Arabidopsis thaliana

Unpublished

3 (bases 1 to 1001)
Brower, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

Direct Submission
Submitted (20-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon B5SRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N120195.

FEATURES
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/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
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/clone="AL022224"
/notes="Derived from superpool 1.28 NASC code N40027"
STs
1..290
/standard_name="SM_3.33484"

ORIGIN
Query Match 10.3%; Score 209; DB 11; Length 290;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1167 TAAATTCAGAGACAAATTAATCAGTTCGTGCTGTTGGAGAGAGAACAGATCAA 1226
Db 209 TAAATTCAGAGACAAATTAATCAGTTCGTGCTGTTGGAGAGAGAACAGATCAA 150

Qy 1227 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAATCT 1286
Db 149 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAATCT 90

Qy 1287 TAAATTAACAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 1346
Db 89 TAAATTAACAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 30

Qy 1347 TTTTAGTTCATGTAATGAATCTGTTTT 1375
Db 29 TTTTAGTTCATGTAATGAATCTGTTTT 1

RESULT 8
AY086004
LOCUS
DEFINITION
Arabidopsis thaliana clone 20592 mRNA, complete sequence.
ACCESSION
AY086004
VERSION
AY086004.1 GI:21404714
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)

2008475
MEDLINE
12093376
PUBMED
2 (bases 1 to 1001)
Brower, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

Full-length cDNA from Arabidopsis thaliana

Unpublished

3 (bases 1 to 1001)
Brower, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

TITLE
JOURNAL

COMMENT
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or LAr ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES
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BEKTELOPKVVEYEAATSAEVALVRDPKVLKNSAAVKYLEELVKIEFPGSKA
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AEPPKP"

CDS
137..811
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AEPPKP"

ORIGIN
Query Match 4.5%; Score 91; DB 8; Length 1001;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1174 AGAGAGACAAATTAATCAGTTTCGTGTGTTGGAGAGAGAGAGACAGATCAATACGAG 1233
DB 1 AGAGAGACAAATTAATCAGTTTCGTGTGTTGGAGAGAGAGAGACAGATCAATACGAG 60
QY 1234 GAGAGATCTCTAAAGAGATTATTCGTTTCAA 1264
DB 61 GAGAGATCTCTAAAGAGATTATTCGTTTCAA 91

RESULT 9
AY093084
LOCUS
DEFINITION
Arabidopsis thaliana endomembrane-associated protein (At4g20260)
mRNA, complete cds.
AY093084
AY093084.1 GI:20260369
FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1070)
Palm, C.J., Bowler, L., Jones, T., Banh, J., Carninci, P., Chen, H.,
Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
Submitted (27-MAR-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,

COMMENT
USA
e-mail for correspondence: arab@sequence.stanford.edu
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFI CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFI cDNAs: Southwick, A., Nguyen, M., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.
FEATURES
Location/Qualifiers
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127..804
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TSGEKEETVEETKKDETETAVVEKPEVEKKEEATPAPAVVETPVKEPTTTTAP
VAEPPKP"

ORIGIN
Query Match 3.9%; Score 79; DB 8; Length 1070;
Best Local Similarity 100.0%; Pred. No. 6.3e-26;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1186 AATCAGTTTCGTGTGTTGGAGAGAGAGAGACAGATCAATACGAGAGATCTCTA 1245
DB 3 AATCAGTTTCGTGTGTTGGAGAGAGAGAGACAGATCAATACGAGAGATCTCTA 62
QY 1246 AAGAGATTATTCGTTTCAA 1264
DB 63 AAGAGATTATTCGTTTCAA 81

RESULT 10
ATENDASPR
LOCUS
DEFINITION
A.thaliana mRNA for endomembrane-associated protein.
Y08061
Y08061.1 GI:1550737
endomembrane-associated protein.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Dupree, P., Prime, T.A. and Packman, L.C.
Sequence of novel endomembrane-associated protein of Arabidopsis thaliana


```
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/protein_id="AAG45205.1"
/db_xref="GI:12007435"
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TTWIFSPFCNPKVHFFCDSPVIALVCADTSVFELEALTATVPILRPPELLILCS
YVRIUSITFRMPSAEGKQAEKSTCSAHLVLSLFTYALTYFRPQSSASSESKLLS
LSSTVTPMLNPILYSSNKEVKAAKRLHRLTIGSQKL"
mRNA
complement(<26726..>27679)
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of this ORF"
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YFFPFGAECCLLATWADRYVAICDPLHVPVIMGHISCAQLAAASWFSFGVATVQ
TTWIFSPFCNPKVHFFCDSPVIALVCADTSVFELEALTATVPILRPPELLILCS
YTHIAAALKTPSAKGNKAFSTCSHLLVLSLFTYALTYFRPQSSASSESKLLS
LSYVTMTMLNPILYSLRNKEVKALSRVTSKALALRNCIP"
32235..32468
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GenBank Accession Number AC017103"
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complement(49988..50941)
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TCASVVAITGAVHMPISAGRYKAFSTCSHLLVLSLFTYALTYFRPQSSASSESKLLS
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deposited in GenBank Accession Number AC024729"
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AHSLL"
ORIGIN
Query Match 1.2%; Score 25; DB 9; Length 111126;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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* 33486 42561: contig of 9076 bp in length
* 42562 42661: gap of unknown length
* 42662 54313: contig of 11652 bp in length
* 54314 54413: gap of unknown length
* 54414 72085: contig of 17672 bp in length
* 72086 72185: gap of unknown length
* 72186 82926: contig of 17111 bp in length
* 82927 89396: gap of unknown length
* 89397 104805: contig of 15409 bp in length
* 104806 121851: gap of unknown length
* 121852 121951: gap of unknown length
* 121952 141389: contig of 19438 bp in length
* 141390 171660: gap of unknown length
* 171660 171660: contig of 30171 bp in length.
FEATURES
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        8183..11955
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            /note="assembly_name:Contig19"

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ORIGIN

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Query Match          1.2%; Score 25; DB 2; Length 171660;
Best Local Similarity 100.0%; Pred.No. 1.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 70 TTCATTACAAAAGGAAAAAATAAT 94
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Db 117997 TTCATTACAAAAGGAAAAAATAAT 117973

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RESULT 14
AC087280
LOCUS          AC087280          173611 bp    DNA    linear    PRI 01-DEC-2001

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DEFINITION

AC087280 Homo sapiens chromosome 11, clone RP11-560B16, complete sequence.
 VERSION AC087280.11 GI:17223193
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 173611)

AUTHORS

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE

Homo sapiens chromosome 11, clone RP11-560B16

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 173611)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B., Brown,A.,
 Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
 Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
 Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
 Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
 McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Norbu C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
 Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
 Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
 Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

Submitted (23-DEC-2000) Whitehead Institute/MIT Center for Genome

JOURNAL

Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 173611)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chararo,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S.,
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Karat,A., Karatas,A., Kells,C., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
 Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome

JOURNAL

Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Dec 1, 2001 this sequence version replaced gi:17047119.

All repeats were identified using RepeatMasker:

Smitt, A.P.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L11843
Center clone name: 560_B_16

FEATURES

source

Location/Qualifiers

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TTCATTACAAAGGAAAAAAAAAT 94

DB 31031 TTCATTACAAAGGAAAAAAAAAT 31055

RESULT 15

AC027641

LOCUS

DEFINITION

AC027641

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC027641

Homo sapiens

SEQUENCE, 18 unordered pieces.

AC027641

AC027641.2

GI:8570385

HTG; HTGS_PHASE1; HTGS_DRAFT.

Homo sapiens (human)

Homo sapiens

208430 bp DNA linear HTG 07-JUL-2000

RP11-732A19, WORKING DRAFT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208430)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 208430)
Waterston,R.H.
Direct Submission
Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 17, 2000 this sequence version replaced gi:7344780.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0732A19
----- Summary Statistics -----
Sequencing vector: M13; 98%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 2% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198825 bases at least Q40
Consensus quality: 202103 bases at least Q30
Consensus quality: 203934 bases at least Q20
Insert size: 219000; agarose-fp
Insert size: 206730; sum-of-contigs
Quality coverage: 4.27 in Q20 bases; agarose-fp
Quality coverage: 4.55 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1760: contig of 1760 bp in length
* 1761 1860: gap of unknown length
* 1861 3171: contig of 1311 bp in length
* 3172 3271: gap of unknown length
* 3272 5628: contig of 2357 bp in length
* 5629 5728: gap of unknown length
* 5729 7760: contig of 2032 bp in length
* 7761 7860: gap of unknown length
* 7861 15503: contig of 7643 bp in length
* 15504 15603: gap of unknown length
* 15604 18871: contig of 3268 bp in length
* 18872 18971: gap of unknown length
* 18972 2430: contig of 3459 bp in length
* 2431 28530: gap of unknown length
* 28531 28556: contig of 6026 bp in length
* 28557 28656: gap of unknown length
* 28657 35414: contig of 6758 bp in length
* 35415 35514: gap of unknown length
* 35515 42738: contig of 7224 bp in length
* 42739 42839: gap of unknown length
* 42839 50307: contig of 7469 bp in length
* 50308 50407: gap of unknown length
* 50408 62974: contig of 12567 bp in length
* 62975 63074: gap of unknown length
* 63075 73753: contig of 10679 bp in length
* 73754 73854: gap of unknown length
* 73854 87630: contig of 13777 bp in length
* 87631 87730: gap of unknown length
* 87731 106802: contig of 19072 bp in length
* 106803 106902: gap of unknown length
* 106903 120650: contig of 13748 bp in length

* 120651 120750: gap of unknown length
* 120751 156637: contig of 35887 bp in length
* 156638 156738: gap of unknown length
* 156738 208430: contig of 51693 bp in length.

FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1-2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 TTCATTACAAAGGAAAAAAT 94
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Db 100281 TTCATTACAAAGGAAAAAAT 100305
|||||

Search completed: October 24, 2005, 04:10:54
Job time : 8849 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 22:06:13 ; Search time 1095 Seconds
(without alignment)
10974.498 Million cell updates/sec

Title: US-10-643-676-1

Perfect score: 2030

Sequence: 1 cttcatgaagatggacca.....ttagattaaacaacaaaaag 2030

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_16Dec04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2030	100.0	2030	6	ABZ75215	Arabidops
2	2030	100.0	2042	6	ABZ75216	Arabidops
3	1064	52.4	1064	6	ABZ16347	Arabidops
4	91	4.5	999	3	AAC49043	Arabidops
5	91	4.5	1001	3	AAC37034	Arabidops
6	89	4.4	495	3	AAC38110	Arabidops
7	83	4.1	515	3	AAC52118	Arabidops
8	53	2.6	1088	6	ABN98348	Arabidops
9	23	1.1	2550	11	ADM03675	Human cDN
10	22	1.1	427	6	ABL98998	Mouse neu
11	22	1.1	427	6	ABL98999	Mouse neu
12	22	1.1	432	4	AAI92210	Human pol
13	22	1.1	468	5	ABV60815	Human pro
14	22	1.1	2115	13	ADS51475	Bacterial
15	22	1.1	9607	2	AAV52213	Streptoco
16	22	1.1	110000	10	AAVS6454_01	Continuation (2 of
17	21	1.0	299	13	ADS51486	Bacterial
18	21	1.0	374	5	ADL41073	Human ova
19	21	1.0	429	4	AAI87584	Human pol
20	21	1.0	549	5	ADL43562	Human ova

c 94	c 20	1.0	15399	6	ABL33514	Abi33514 Human imm	c 167	19	0.9	767	6	ABQ21779	Abq21779 Oligonucle
c 95	c 20	1.0	16918	6	ABL33617	Abi33617 Human imm	c 168	19	0.9	801	13	ADR05448	Adr05448 Hra3-C cd
c 96	c 20	1.0	22660	4	ABL09700	Abi09700 Drosophil	c 169	19	0.9	844	3	AAA26705	Aaa26705 Candida a
c 97	c 20	1.0	50657	13	ABD33455	Abd33455 Murine ca	c 170	19	0.9	845	2	AAT11323	Aat11323 DNA encod
c 98	c 20	1.0	60604	12	ADO48003	Ado48003 Human HIP	c 171	19	0.9	858	4	ABL10365	Abi10365 Drosophil
c 99	c 20	1.0	70708	12	ADQ97605	Adq97605 Human can	c 172	19	0.9	930	6	ABN93296	Abn93296 Staphyloc
c 100	c 20	1.0	77777	12	ADQ94674	Adq94674 Human chr	c 173	19	0.9	930	13	ADS04288	Ads04288 Staphyloc
c 101	c 20	1.0	84476	12	ADQ97028	Adq97028 Human can	c 174	19	0.9	955	6	AAI69492	Aai69492 A. sulcat
c 102	c 20	1.0	103929	3	AAF22287	Aaf22287 BAC conta	c 175	19	0.9	979	4	AAK61948	Aak61948 Human imm
c 103	c 20	1.0	110000	3	AAF22305_03	Continuation (4 of	c 176	19	0.9	1019	3	AAC96901	Aac96901 Arabidops
c 104	c 20	1.0	110000	13	ABD32905_6	Continuation (7 of	c 177	19	0.9	1033	6	ABN98420	Abn98420 Arabidops
c 105	c 20	1.0	117754	11	ACN43866	Acn43866 Human gen	c 178	19	0.9	1038	6	ABN98420	Abn98420 Arabidops
c 106	c 20	1.0	122937	13	ABD33516	Abd33516 Human can	c 179	19	0.9	1040	9	ADN15602	Adn15602 DNA encod
c 107	c 20	1.0	160771	16	AQ888179	Aq888179 Human ost	c 180	19	0.9	1040	10	ADD55851	Add55851 Thalecres
c 108	c 20	1.0	204621	11	ACN44486	Acn44486 Human gen	c 181	19	0.9	1040	12	ADOO1928	Adoo1928 Thalecres
c 109	c 20	1.0	225587	12	ADQ97397	Adq97397 Human can	c 182	19	0.9	1044	6	ABK95353	Abk95353 DNA encod
c 110	c 20	1.0	260803	13	ABD32730	Abd32730 Human can	c 183	19	0.9	1111	10	ADE53764	Ades3764 Human pro
c 111	c 19	0.9	100	10	ADG70320	Adg70320 ANGE 1 SN	c 184	19	0.9	1154	3	AAC44106	Aac44106 Arabidops
c 112	c 19	0.9	100	10	ADG70323	Adg70323 ANGE 1 SN	c 185	19	0.9	1172	13	ADS05053	Ads05053 Bacterial
c 113	c 19	0.9	103	6	ABK80027	Abk80027 Bacillus	c 186	19	0.9	1228	3	AAQ79775	Aaq79775 Human sec
c 114	c 19	0.9	140	3	AAC29478	Aac29478 Human sec	c 187	19	0.9	1327	12	ADK67712	Adk67712 Human mod
c 115	c 19	0.9	225	3	AAC41824	Aac41824 Arabidops	c 188	19	0.9	1337	12	ADJ27248	Adj27248 Human TRI
c 116	c 19	0.9	277	13	ACN52665	Acn52665 Corton an	c 189	19	0.9	1447	2	AAZ77457	Aaz77457 Human ova
c 117	c 19	0.9	289	4	AAI88427	Aai88427 Human pol	c 190	19	0.9	1451	6	ABK33940	Abk33940 Human DNA
c 118	c 19	0.9	343	10	ADD16308	Add16308 DNA (SeqI	c 191	19	0.9	1451	8	ADA20398	Ada20398 Prostate
c 119	c 19	0.9	352	6	ABL82126	Abi82126 Human ova	c 192	19	0.9	1451	8	ADAB4205	Ada84205 Human ren
c 120	c 19	0.9	352	8	ABX44964	Abx44964 Bovine ES	c 193	19	0.9	1478	3	AAZ51628	Aaz51628 Human mem
c 121	c 19	0.9	355	5	ABV61297	Abv61297 Human pro	c 194	19	0.9	1487	13	ADR83552	Adr83552 Murine HE
c 122	c 19	0.9	362	4	AAI83208	Aai83208 Human pol	c 195	19	0.9	1609	13	ADR05475	Adr05475 HTA3-G ge
c 123	c 19	0.9	369	4	AAI87529	Aai87529 Human pol	c 196	19	0.9	1666	8	ACC72435	Acc72435 Human sec
c 124	c 19	0.9	375	4	AAI89598	Aai89598 Human pol	c 197	19	0.9	1782	6	ABN79798	Abn79798 Fungal ZB
c 125	c 19	0.9	381	5	ABV61901	Abv61901 Human pro	c 198	19	0.9	1789	2	AAQ99226	Aaq99226 Braesica
c 126	c 19	0.9	389	4	AAI87676	Aai87676 Human pol	c 199	19	0.9	1803	2	AAV31257	Aav31257 E. coli J
c 127	c 19	0.9	389	9	ACH29275	Ach29275 Human adu	c 200	19	0.9	1821	2	AAV22736	Aav22736 Babesia m
c 128	c 19	0.9	398	13	ACN53082	Acn53082 Corton an	c 201	19	0.9	1821	2	AAH89000	Aah89000 Babesia m
c 129	c 19	0.9	399	4	AAI93256	Aai93256 Human pol	c 202	19	0.9	1821	3	AAQ65083	Aaq65083 B. microt
c 130	c 19	0.9	403	10	ADC72604	Adc72604 DNA Seq I	c 203	19	0.9	1821	6	ABL89327	Abi89327 Babesia m
c 131	c 19	0.9	403	10	ADC72358	Adc72358 DNA Seq I	c 204	19	0.9	1821	8	ACA92622	ACA92622 DNA encod
c 132	c 19	0.9	403	10	ADD17185	Add17185 DNA (SeqI	c 205	19	0.9	1832	10	ADE06189	Ade06189 BWNI-rela
c 133	c 19	0.9	403	10	ADK59047	Adk59047 Plant DNA	c 206	19	0.9	1832	3	AAQ42640	Aaq42640 Arabidops
c 134	c 19	0.9	405	9	ACH18141	Ach18141 Human adu	c 207	19	0.9	1868	6	ABZ17263	Abz17263 Arabidops
c 135	c 19	0.9	413	5	ABV60954	Abv60954 Human pro	c 208	19	0.9	2000	8	ADA72550	Ada72550 Rice gene
c 136	c 19	0.9	418	4	AAI86360	Aai86360 Human pol	c 209	19	0.9	2033	3	AAQ40796	Aaq40796 Arabidops
c 137	c 19	0.9	419	9	ACH50072	Ach50072 Human leu	c 210	19	0.9	2135	6	ABK99840	Abk99840 Babesia c
c 138	c 19	0.9	432	4	AAI89198	Aai89198 Human pol	c 211	19	0.9	2310	2	AAQ25546	Aaq25546 Arabidops
c 139	c 19	0.9	434	6	AAI23097	Aai23097 Human bre	c 212	19	0.9	2442	4	AAI69728	Aai69728 Microtubu
c 140	c 19	0.9	436	6	ABL87388	Abi87388 Human ova	c 213	19	0.9	2639	4	ABL02633	Abi02633 Drosophil
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c 144	c 19	0.9	451	11	ADM65271	Adm65271 Human Y c	c 217	19	0.9	2933	10	ADE56136	Ade56136 Rat gene
c 145	c 19	0.9	461	2	AAV99639	Aav99639 Human t-p	c 218	19	0.9	2933	10	ADE56140	Ade56140 Rat gene
c 146	c 19	0.9	480	5	ABV10746	Abv10746 Human pro	c 219	19	0.9	2933	10	ADE56128	Ade56128 Rat gene
c 147	c 19	0.9	486	6	ABK74683	Abk74683 Bacillus	c 220	19	0.9	2970	13	ADRS8928	Adrs8928 Human Elk
c 148	c 19	0.9	501	6	ABN93117	Abn93117 Staphyloc	c 221	19	0.9	2981	10	ADE56120	Ade56120 Rat gene
c 149	c 19	0.9	501	13	ADS03995	Ads03995 Staphyloc	c 222	19	0.9	3047	4	AAH15890	Aah15890 Human CDN
c 150	c 19	0.9	507	5	ADL45017	Adl45017 Human ova	c 223	19	0.9	3047	4	AAH77801	Aah77801 Nucleotid
c 151	c 19	0.9	513	4	AAI86094	Aai86094 Human pol	c 224	19	0.9	3107	6	ABK33997	Abk33997 Human DNA
c 152	c 19	0.9	519	10	ADH84275	Adh84275 Enterococ	c 225	19	0.9	3107	8	ADA20429	Ada20429 Prostate
c 153	c 19	0.9	564	6	ABQ19371	Abq19371 Oligonuc	c 226	19	0.9	3107	8	ADA84236	Ada84236 Human ren
c 154	c 19	0.9	564	6	ABQ19370	Abq19370 Oligonuc	c 227	19	0.9	3374	4	ABL26932	Abi26932 Drosophil
c 155	c 19	0.9	566	5	ABV51724	Abv51724 Human pro	c 228	19	0.9	3410	4	AAH54074	Aah54074 S. epider
c 156	c 19	0.9	573	12	ADN74834	Adn74834 Thale cre	c 229	19	0.9	3474	6	AAH54494	Aah54494 S. epider
c 157	c 19	0.9	578	12	ACH73095	Ach73095 Human gen	c 230	19	0.9	3948	6	ABZ11243	Abz11243 Human pol
c 158	c 19	0.9	594	3	AAQ54122	Aaq54122 Arabidops	c 231	19	0.9	3948	12	ADM43761	Adm43761 Novel hum
c 159	c 19	0.9	596	6	ABN60109	Abn60109 Human can	c 232	19	0.9	4223	2	AAV22752	Aav22752 Babesia m
c 160	c 19	0.9	623	3	AAQ35048	Aaq35048 Arabidops	c 233	19	0.9	4223	2	AAV22737	Aav22737 Babesia m
c 161	c 19	0.9	631	6	ABQ52849	Abq52849 Oligonuc	c 234	19	0.9	4223	2	AAQ90001	Aaq90001 Babesia m
c 162	c 19	0.9	631	6	ABQ52848	Abq52848 Oligonuc	c 235	19	0.9	4223	2	AAQ90015	Aaq90015 Babesia m
c 163	c 19	0.9	664	4	AAK71302	Aak71302 Human imm	c 236	19	0.9	4223	3	AAQ65098	Aaq65098 B. microt
c 164	c 19	0.9	696	11	ACN91654	Acn91654 Breast ca	c 237	19	0.9	4223	3	AAQ65084	Aaq65084 B. microt
c 165	c 19	0.9	744	2	AAQ20367	Aaq20367 Borrelia	c 238	19	0.9	4223	6	ABL89342	Abi89342 Babesia m
c 166	c 19	0.9	767	6	ABQ21778	Abq21778 Oligonuc	c 239	19	0.9	4223	6	ABL89328	Abi89328 Babesia m

240	19	0.9	4223	8	ACA92623	AcA92623 DNA encod	313	19	0.9	17421	4	AAS45349	Aas45349 Chemical
c 241	19	0.9	4223	8	ACA92637	AcA92637 B. microt	c 314	19	0.9	17421	4	AAS45349	Aas45349 Chemical
c 242	19	0.9	4223	10	ADE05991	Ade05991 BMDI-rela	c 315	19	0.9	17421	6	ABK28182	Abk28182 DNA trans
c 243	19	0.9	4223	10	ADE06190	Ade06190 BMDI-rela	c 316	19	0.9	17421	6	ABK28182	Abk28182 DNA trans
c 244	19	0.9	4945	4	ABL02632	AbL02632 Drosophil	c 317	19	0.9	17421	6	ABL34574	AbL34574 Human met
c 245	19	0.9	5129	12	ADM67113	Adm67113 Human hom	c 318	19	0.9	17491	7	ADN99835	Adn99835 Bisulphit
c 246	19	0.9	5129	13	ADR99019	Adr99019 Rab3 GTPa	c 319	19	0.9	17534	6	ABK40026	Abk40026 Human che
c 247	19	0.9	5338	6	ABK31379	Abk31379 Signal tr	c 320	19	0.9	17721	6	ABL33728	AbL33728 Human inm
c 248	19	0.9	5338	6	ABL70330	AbL70330 Chemical	c 321	19	0.9	17970	6	ABQ67034	AbQ67034 Human ang
c 249	19	0.9	5338	6	AAS61281	Aas61281 Human gen	c 322	19	0.9	18133	6	ABK40017	Abk40017 Human che
c 250	19	0.9	5442	6	ABL33968	AbL33968 Human inm	c 323	19	0.9	18133	6	ABL32940	AbL32940 Human inm
c 251	19	0.9	5569	4	ABL10364	AbL10364 Drosophil	c 324	19	0.9	18357	6	ABQ67084	AbQ67084 Human ang
c 252	19	0.9	5807	6	ABL33154	AbL33154 Human inm	c 325	19	0.9	19441	4	AAK80351	Aak80351 Human inm
c 253	19	0.9	6047	6	ABL33459	AbL33459 Human inm	c 326	19	0.9	21500	11	ACN43960	Acn43960 Mouse gen
c 254	19	0.9	6126	6	ABL33445	AbL33445 Human inm	c 327	19	0.9	25179	13	ABD33248	Abd33248 Murine ca
c 255	19	0.9	6126	6	ABL33445	AbL33445 Human inm	c 328	19	0.9	28118	10	ADE43798	Ade43798 Polymorph
c 256	19	0.9	6126	6	ABL331335	Abk31335 Signal tr	c 329	19	0.9	28118	10	ADH54276	Adh54276 Human TNF
c 257	19	0.9	6215	6	ABL33190	AbL33190 Human inm	c 330	19	0.9	28118	12	ADH54275	Adh54275 Human TNF
c 258	19	0.9	6240	6	ABL32137	AbL32137 Human inm	c 331	19	0.9	29993	10	ADB37663	Adb37663 Human che
c 259	19	0.9	6240	6	ABL32455	AbL32455 Human met	c 332	19	0.9	29993	10	ADB37661	Adb37661 Human che
c 260	19	0.9	6240	7	ADS99716	AdS99716 Complemen	c 333	19	0.9	38342	4	AAS46746	Aas46746 Tumour su
c 261	19	0.9	6270	6	ABL33873	AbL33873 Human inm	c 334	19	0.9	38342	6	ABK31507	Abk31507 Signal tr
c 262	19	0.9	6837	6	AAD29902	Aad29902 Plasmid p	c 335	19	0.9	45121	9	ADA02744	Ada02744 Human TNF
c 263	19	0.9	6866	6	ABL32667	AbL32667 Human inm	c 336	19	0.9	45121	10	ADB72482	Adb72482 Human TNF
c 264	19	0.9	6866	6	ABL49320	AbL49320 Human pol	c 337	19	0.9	45121	10	ADC85224	Adc85224 Human trf
c 265	19	0.9	6888	6	ABL34441	AbL34441 Human inm	c 338	19	0.9	45121	10	ADM74339	Adm74339 Human car
c 266	19	0.9	7058	6	ABK40051	Abk40051 Human che	c 339	19	0.9	45121	12	ADM74339	Adm74339 Human car
c 267	19	0.9	7083	4	ABL02670	AbL02670 Drosophil	c 340	19	0.9	52616	4	AAK70459	Aak70459 Human inm
c 268	19	0.9	7322	11	ACN92378	AcN92378 Breast ca	c 341	19	0.9	52616	4	AAK70459	Aak70459 Human inm
c 269	19	0.9	7522	6	ABL32915	AbL32915 Human inm	c 342	19	0.9	55829	13	ABD33512	Abd33512 Human can
c 270	19	0.9	7544	4	AAS45301	Aas45301 Chemical	c 343	19	0.9	60500	11	ACN44530	Acn44530 Human gen
c 271	19	0.9	7544	6	ABK28140	Abk28140 DNA trans	c 344	19	0.9	65464	8	ABX13172	Abx13172 Human gen
c 272	19	0.9	7832	6	ABK67847	Abk67847 Lettuce p	c 345	19	0.9	68004	6	ABL57909	AbL57909 3
c 273	19	0.9	8103	6	ABL33661	AbL33661 Human inm	c 346	19	0.9	71578	11	ACN44284	Acn44284 Mouse gen
c 274	19	0.9	8168	6	ABL32929	AbL32929 Human inm	c 347	19	0.9	73334	6	ABL34124	AbL34124 Human inm
c 275	19	0.9	8168	6	ABL32929	AbL32929 Human inm	c 348	19	0.9	73334	6	ABL592318	AbL592318 Human can
c 276	19	0.9	8168	6	AAS63328	Aas63328 Chemical	c 349	19	0.9	73742	12	ADQ97824	Adq97824 Human can
c 277	19	0.9	8168	6	AAS63329	Aas63329 Chemical	c 350	19	0.9	76416	10	ADL13662	Adl13662 Osteoarth
c 278	19	0.9	8514	4	AAK81530	Aak81530 Human inm	c 351	19	0.9	76600	12	ADO79402	Ado79402 DLGI regi
c 279	19	0.9	8530	6	ABL32432	AbL32432 Human inm	c 352	19	0.9	82938	6	ABV72623	Abv72623 Human tra
c 280	19	0.9	8758	6	ABL33118	AbL33118 Human inm	c 353	19	0.9	83180	11	ACN44784	Acn44784 Mouse gen
c 281	19	0.9	8758	6	ABL34076	AbL34076 Human inm	c 354	19	0.9	90220	11	ABK83576	Abk83576 Human cdn
c 282	19	0.9	8915	4	ABL29664	AbL29664 Drosophil	c 355	19	0.9	93483	9	ADA03083	Ada03083 Mouse mCG
c 283	19	0.9	9390	4	ABL13248	AbL13248 Drosophil	c 356	19	0.9	93483	9	ADA66367	Ada66367 Mouse mCG
c 284	19	0.9	9728	6	ABK40092	Abk40092 Human che	c 357	19	0.9	93483	10	ADB72821	Adb72821 Mouse mCG
c 285	19	0.9	9728	6	ABL33903	AbL33903 Human inm	c 358	19	0.9	93483	11	ADL27161	Adl27161 Mouse gen
c 286	19	0.9	9914	4	ABK42671	Abk42671 Genomic s	c 359	19	0.9	95835	11	ACN45042	Acn45042 Human gen
c 287	19	0.9	9914	9	ADB60827	AdB60827 Connectiv	c 360	19	0.9	96594	10	ADE95974	Ade95974 Human gen
c 288	19	0.9	9963	6	ABL32695	AbL32695 Human inm	c 361	19	0.9	96594	9	ADA02726	Ada02726 Human SYK
c 289	19	0.9	10250	6	ABN80083	Abn80083 Human che	c 362	19	0.9	96595	10	ADB72464	Adb72464 Human SYK
c 290	19	0.9	10528	6	ABL32335	AbL32335 Human inm	c 363	19	0.9	96960	8	ACF62734	Acf62734 Cancer ba
c 291	19	0.9	10815	2	AAV441199	Aav441199 Lettuce r	c 364	19	0.9	96960	8	ADJ20849	Adj20849 MRP1 base
c 292	19	0.9	10815	6	ABK67796	Abk67796 Lettuce p	c 365	19	0.9	96960	10	ABN87938	Abn87938 Human UGT
c 293	19	0.9	11049	6	ABL92221	AbL92221 Chemical	c 366	19	0.9	96960	10	ABD96921	Abd96921 Human MDR
c 294	19	0.9	11049	6	ABL49324	AbL49324 Human pol	c 367	19	0.9	96960	10	ADJ92112	Adj92112 Human MDR
c 295	19	0.9	11670	6	ABL54325	AbL54325 Chemical	c 368	19	0.9	98844	7	ADJ84099	Adj84099 Human WRN
c 296	19	0.9	12816	4	ABL20852	AbL20852 Drosophil	c 369	19	0.9	100000	6	ABQ74541	Abq74541 Human tra
c 297	19	0.9	12986	4	AAS46554	Aas46554 Tumour su	c 370	19	0.9	107280	13	ABD33169	Abd33169 Murine ca
c 298	19	0.9	13149	2	AAV44231	Aav44231 Lettuce r	c 371	19	0.9	107856	13	ABD32933	Abd32933 Mouse can
c 299	19	0.9	13149	6	ABK67843	Abk67843 Lettuce p	c 372	19	0.9	110000	2	AAT58840	Aat58840 Mycoplasma
c 300	19	0.9	13339	2	AAV44234	Aav44234 Lettuce p	c 373	19	0.9	110000	6	ABX08336	Abx08336 14
c 301	19	0.9	13449	6	ABL33385	AbL33385 Human inm	c 374	19	0.9	110000	10	ABG70447	Abg70447 3
c 302	19	0.9	14491	8	ABZ10061	Abz10061 Haematopo	c 375	19	0.9	110000	10	ABG79565	Abg79565 3
c 303	19	0.9	14491	8	ABZ10207	Abz10207 Haematopo	c 376	19	0.9	110000	11	ACN43998	Acn43998 3
c 304	19	0.9	14491	13	ADS89667	AdS89667 Oligonucle	c 377	19	0.9	110000	11	ACN43998	Acn43998 3
c 305	19	0.9	14913	13	ADS89393	AdS89393 Oligonucle	c 378	19	0.9	110000	12	ADJ25985	Adj25985 14
c 306	19	0.9	15122	6	ABL32775	AbL32775 Human inm	c 379	19	0.9	110000	12	ADN97989	Adn97989 14
c 307	19	0.9	15861	6	ABL32524	AbL32524 Human inm	c 380	19	0.9	119950	2	AAX90201	Aax90201 Human Yeg
c 308	19	0.9	16127	6	ABL32745	AbL32745 Human inm	c 381	19	0.9	122923	11	ACN44026	Acn44026 Human gen
c 309	19	0.9	16173	6	ABL34468	AbL34468 Human met	c 382	19	0.9	143412	11	ACN44512	Acn44512 Mouse gen
c 310	19	0.9	16173	7	ADS99729	AdS99729 Bisulphit	c 383	19	0.9	145985	12	ADQ97164	Adq97164 Human can
c 311	19	0.9	16688	4	AAS46555	Aas46555 Tumour su	c 384	19	0.9	145985	12	ADQ97164	Adq97164 Human can
c 312	19	0.9	17141	6	AAD26486	Aad26486 Bovine ga	c 385	19	0.9	146733	12	ADQ97410	Adq97410 Mouse can

c 386	19	0.9	150830	12	ADQ97260	Adq97260 Mouse can	c 459	18	0.9	380	4	AAI88638	Aai88638 Human pol
c 387	19	0.9	152501	12	ADP67269	Adp67269 Human chr	460	18	0.9	384	6	ABQ85232	Abq85232 Arabidops
388	19	0.9	154465	6	AAD28763	Aad28763 Human AKA	c 461	18	0.9	385	5	ADI74507	Adi74507 Human ova
389	19	0.9	158245	6	ADAD28762	Adad28762 Human AKA	c 462	18	0.9	385	5	ADI68136	Adi68136 Human ova
390	19	0.9	161425	4	AAH02340	Aah02340 Human AKA	c 463	18	0.9	390	4	AAS24796	Aae24796 Human ova
391	19	0.9	161425	4	AAH02340	Aah02340 Human AKA	c 464	18	0.9	390	4	AAS25234	Aae25234 Human ova
392	19	0.9	162025	6	ADAD28758	Adad28758 Human AKA	c 465	18	0.9	391	5	ABV37425	Abv37425 Human pro
393	19	0.9	162025	6	ADAD28759	Adad28759 Human AKA	466	18	0.9	393	5	ADI74443	Adi74443 Human ova
394	19	0.9	162025	13	ADS75958	Ads75958 Human A-k	467	18	0.9	393	5	ADI68071	Adi68071 Human ova
395	19	0.9	162025	13	ADS75958	Ads75958 Human A-k	468	18	0.9	394	5	ADI74256	Adi74256 Human ova
396	19	0.9	162025	13	ADS75963	Ads75963 Human A-k	469	18	0.9	394	5	ADI67879	Adi67879 Human ova
397	19	0.9	162025	13	ADS75962	Ads75962 Human A-k	470	18	0.9	396	5	ABV00134	Abv00134 Human pro
c 398	19	0.9	171324	11	ACN43892	Acn43892 Mouse gen	c 471	18	0.9	397	4	AAS24967	Aae24967 Human ova
c 399	19	0.9	177866	10	ADL13935	Adl13935 Osteoarth	472	18	0.9	398	4	AAS25164	Aae25164 Human ova
c 400	19	0.9	180227	13	ABD33268	Abd33268 Human can	473	18	0.9	400	5	ABV47292	Abv47292 Human pro
c 401	19	0.9	180550	10	ADL133850	Adl133850 Osteoarth	474	18	0.9	401	4	AAI87600	Aai87600 Human pol
c 402	19	0.9	198285	6	ABK84659	Abk84659 Human cdn	c 475	18	0.9	402	6	ABN94866	Abn94866 Gene #136
c 403	19	0.9	198285	6	ABN97319	Abn97319 Gene #381	476	18	0.9	404	4	AAI92214	Aai92214 Human pol
c 404	19	0.9	198285	13	ADR52987	Adr52987 Drug thr	c 477	18	0.9	404	9	ACH21593	Ach21593 Human adu
405	19	0.9	224112	13	ABD32600	Abd32600 Mouse can	478	18	0.9	407	8	ABX62545	Abx62545 Arabidops
406	19	0.9	235033	2	AAV57926	Aav57926 Hereditar	c 479	18	0.9	408	9	ACH16506	Ach16506 Human adu
407	19	0.9	237326	2	AAV57903	Aav57903 Hereditar	480	18	0.9	408	13	ACN56309	Acn56309 Cotton an
c 408	19	0.9	277616	13	ABD32602	Abd32602 Human can	c 481	18	0.9	409	5	ADL43419	Adl43419 Human ova
c 409	19	0.9	290547	13	ABD32598	Abd32598 Human can	482	18	0.9	409	9	ACH16770	Ach16770 Human adu
c 410	19	0.9	304326	13	ADS15253	Ads15253 Rat senso	c 483	18	0.9	410	5	ABV56396	Abv56396 Human pro
c 411	19	0.9	304905	11	ADP75180	Adp75180 Human end	484	18	0.9	412	4	AAK60606	Aak60606 Human mm
c 412	19	0.9	330973	11	ACN44846	Acn44846 Human gen	c 485	18	0.9	412	4	AAI93150	Aai93150 Human pol
413	18	0.9	50	4	AAI74541	Aai74541 Human g11	486	18	0.9	415	5	ADI70165	Adi70165 Human ova
414	18	0.9	51	4	AAL29390	Aal29390 Human SNP	487	18	0.9	415	5	ADI76494	Aai76494 Human ova
415	18	0.9	51	4	AAL29391	Aal29391 Human SNP	c 488	18	0.9	416	4	AAI86045	Aai86045 Human pol
c 416	18	0.9	64	2	ATAT23945	Aat23945 Human gen	489	18	0.9	416	6	ABV94293	Abv94293 Breast ca
c 417	18	0.9	153	13	ACN61614	Acn61614 Cotton gy	490	18	0.9	418	5	ABV02253	Abv02253 Human pro
c 418	18	0.9	169	3	AAA44502	Aaa44502 Human sec	c 491	18	0.9	423	10	ADB56582	Adb56582 Toxicity-
c 419	18	0.9	171	6	ABN70060	Abn70060 Streptoco	c 492	18	0.9	423	12	ADP72059	Adp72059 Renal tox
c 420	18	0.9	174	4	AAL04406	Aal04406 Human tep	c 493	18	0.9	426	5	ADL44606	Adl44606 Human ova
c 421	18	0.9	174	10	ABX61003	Abx61003 Arabidops	c 494	18	0.9	428	5	ABV14216	Abv14216 Human pro
c 422	18	0.9	195	6	ADH31656	Adh31656 Novel yea	c 495	18	0.9	430	4	AAI85300	Aai85300 Human pol
c 423	18	0.9	206	6	ABN20116	Abn20116 Human ORF	c 496	18	0.9	430	4	ACH19136	Ach19136 Human adu
424	18	0.9	217	3	ACAC22600	Aac22600 Human sec	497	18	0.9	432	8	ABX61999	Abx61999 Arabidops
425	18	0.9	218	12	ACH90719	Ach90719 Human gen	498	18	0.9	434	6	ABX69631	Abx69631 Novel mur
426	18	0.9	231	6	ABN72980	Abn72980 Clone 077	c 499	18	0.9	434	8	ABX38360	Abx38360 Bovine ES
427	18	0.9	231	9	ADA08621	Ada08621 Human 077	c 500	18	0.9	435	5	ADL39641	Adl39641 Human ova
428	18	0.9	231	10	ADP08964	Adp08964 CDNA enco	c 501	18	0.9	441	5	ADL39738	Adl39738 Human ova
429	18	0.9	238	10	ABX83935	Abx83935 Corn ear-	c 502	18	0.9	441	5	ADL392484	Adl392484 Human pol
c 430	18	0.9	246	6	ABN91640	Abn91640 Staphyloc	503	18	0.9	444	1	AAAN91069	Aaan91069 Cloned CD
c 431	18	0.9	246	13	ADS02669	Ads02669 Staphyloc	504	18	0.9	444	5	ADI75137	Adi75137 Human ova
432	18	0.9	258	4	AAK57482	Aak57482 Human mm	505	18	0.9	444	5	ADI68778	Adi68778 Human ova
c 433	18	0.9	269	3	AAA41830	Aaa41830 Human sec	c 506	18	0.9	445	8	ABX54049	Abx54049 Bovine ES
c 434	18	0.9	287	12	ADP92817	Adp92817 Cotton ex	507	18	0.9	445	5	ADI68761	Adi68761 Human ova
435	18	0.9	302	9	ACC72342	Acc72342 Human cdn	508	18	0.9	446	5	ADI75120	Adi75120 Human ova
436	18	0.9	315	4	AAI91643	Aai91643 Human pol	509	18	0.9	446	10	ADH69123	Adh69123 Human tum
437	18	0.9	316	6	ABN75585	Abn75585 Human ORF	c 510	18	0.9	447	5	ABV05047	Abv05047 Human pro
c 438	18	0.9	330	5	ADI71884	Adi71884 Human ova	c 511	18	0.9	448	4	AAS24989	Aae24989 Human ova
c 439	18	0.9	330	5	ADL37035	Adl37035 Human ova	512	18	0.9	448	13	ACN56120	Acn56120 Cotton an
c 440	18	0.9	333	5	ABV61653	Abv61653 Human pro	513	18	0.9	456	5	ABV09280	Abv09280 Human pro
c 441	18	0.9	336	6	ABN91228	Abn91228 Staphyloc	514	18	0.9	462	5	ADI68152	Adi68152 Human ova
c 442	18	0.9	336	13	ADS01437	Ads01437 Staphyloc	515	18	0.9	462	5	ADI74523	Adi74523 Human ova
443	18	0.9	339	5	ABV12927	Abv12927 Human pro	516	18	0.9	462	9	ACH26701	Ach26701 Human adu
c 444	18	0.9	339	6	ABN90677	Abn90677 Staphyloc	517	18	0.9	463	5	ABV30456	Abv30456 Human pro
c 445	18	0.9	339	13	ADS03881	Ads03881 Staphyloc	518	18	0.9	463	5	ADI68779	Adi68779 Human ova
c 446	18	0.9	343	4	AAI88988	Aai88988 Human pol	519	18	0.9	463	5	ADI75138	Adi75138 Human ova
447	18	0.9	353	4	AAAS38160	Aaas38160 Novel hum	520	18	0.9	463	10	ADH69126	Adh69126 Human tum
448	18	0.9	357	4	AAK90758	Aak90758 Human dig	521	18	0.9	464	4	AAI15472	Aai15472 Probe #54
449	18	0.9	357	4	AAK90757	Aak90757 Human dig	522	18	0.9	464	4	ABAS7311	Abas7311 Human toe
450	18	0.9	357	4	AAK90760	Aak90760 Human dig	523	18	0.9	464	4	AAI36853	Aai36853 Probe #55
451	18	0.9	357	2	AAV70867	Aav70867 Internal	524	18	0.9	464	4	ABA26863	Abas26863 Probe #53
452	18	0.9	366	5	ABV03758	Abv03758 Human pro	525	18	0.9	464	4	AAK30940	Aak30940 Human bon
c 453	18	0.9	366	9	ACH42695	Ach42695 Human pro	526	18	0.9	464	4	AAK05346	Aak05346 Human bra
454	18	0.9	367	5	ABV11422	Abv11422 Human toe	527	18	0.9	464	4	ABS30618	Abs30618 Human liv
455	18	0.9	368	6	ABN73683	Abn73683 Bovine em	528	18	0.9	464	6	ABS05688	Abs05688 Human gen
456	18	0.9	369	3	AAC20944	Aac20944 Human sec	c 529	18	0.9	465	4	AAS24842	Aas24842 Human ova
457	18	0.9	369	6	ABK76527	Abk76527 Bacillus	c 530	18	0.9	465	4	AAAS25281	Aas25281 Human ova
c 458	18	0.9	373	10	ADI81900	Adi81900 A. thalia	531	18	0.9	466	5	ADI68707	Adi68707 Human ova

532	18	0.9	466	5	ADI75068	Adi75068 Human ova	605	18	0.9	557	5	ABV41361	Abv41361 Human pro
533	18	0.9	467	5	ADI75039	Adi75039 Human ova	606	18	0.9	557	5	ABV44061	Abv44061 Human pro
534	18	0.9	467	5	ADI68677	Adi68677 Human ova	607	18	0.9	557	5	ADL42218	Adl42218 Human ova
535	18	0.9	468	5	ABV56200	Abv56200 Human pro	608	18	0.9	558	5	ADL40284	Adl40284 Human ova
536	18	0.9	469	5	ADL39744	Adl39744 Human ova	c 609	18	0.9	561	4	AA525018	Aa525018 Human ova
537	18	0.9	470	3	AAC37252	Aac37252 Arabidops	c 610	18	0.9	561	12	ADO63628	Ado63628 Tranecrip
538	18	0.9	470	5	ABV42919	Abv42919 Human pro	c 611	18	0.9	571	5	AAH83634	Aah83634 Human ova
539	18	0.9	470	5	ABV34052	Abv34052 Human pro	c 612	18	0.9	571	5	ABV35222	Abv35222 Human pro
540	18	0.9	470	5	ABV41492	Abv41492 Human pro	c 613	18	0.9	573	4	AAH29095	Aah29095 Drosophil
541	18	0.9	470	5	ABV32567	Abv32567 Human pro	c 614	18	0.9	573	5	ADL40303	Adl40303 Human ova
542	18	0.9	470	5	ADI67875	Adi67875 Human ova	615	18	0.9	573	8	ACA39244	Aca39244 Prokaryot
543	18	0.9	470	5	ADL74252	Adl74252 Human ova	616	18	0.9	574	4	ABA88607	Ab88607 Escherich
544	18	0.9	477	5	ADL40365	Adl40365 Human ova	617	18	0.9	575	8	ABZ75570	Abz75570 Rice albu
545	18	0.9	478	9	ACH48211	Ach48211 Human lun	618	18	0.9	583	5	ADL40276	Adl40276 Human ova
546	18	0.9	479	5	ABV35310	Abv35310 Human pro	619	18	0.9	587	6	ABO20070	Abg20070 Oligonuel
547	18	0.9	479	5	ABV44142	Abv44142 Human pro	c 620	18	0.9	587	6	ABO20071	Abg20071 Oligonuel
548	18	0.9	480	4	AA524748	Aa524748 Human ova	c 621	18	0.9	588	6	ABQ52101	Abq52101 Oligonuel
549	18	0.9	480	5	AAH83378	Aah83378 Human ova	c 622	18	0.9	588	6	ABQ52100	Abq52100 Oligonuel
550	18	0.9	480	5	ADL38878	Adl38878 Human ova	c 623	18	0.9	594	4	AAK88246	Aak88246 Human dig
551	18	0.9	481	5	ADL72202	Adl72202 Human ova	c 624	18	0.9	594	5	AA539398	Aa539398 cDNA enco
552	18	0.9	482	5	ABV49155	Abv49155 Human pro	c 625	18	0.9	594	9	ADB32124	Adb32124 Human nov
553	18	0.9	483	12	ADQ18576	Adq18576 Human sof	c 626	18	0.9	594	12	ACH77007	Ach77007 Human gen
554	18	0.9	485	5	AAH83479	Aah83479 Human ova	c 627	18	0.9	595	5	AAH55848	Aah55848 Human SCN
555	18	0.9	485	6	AA561517	Aa561517 Lung smal	c 628	18	0.9	598	10	ADK54516	Adk54516 Planc DNA
556	18	0.9	486	5	ADL39760	Adl39760 Human ova	629	18	0.9	600	5	ABV14127	Abv14127 Human pro
557	18	0.9	486	5	ADI68705	Adi68705 Human ova	630	18	0.9	601	5	ABV11286	Abv11286 Human pro
558	18	0.9	488	5	ADI75066	Adi75066 Human ova	c 631	18	0.9	602	6	ABO50531	Abg50531 Oligonuel
559	18	0.9	488	5	ADI75148	Adi75148 Human ova	632	18	0.9	602	6	ABQ50530	Abq50530 Oligonuel
560	18	0.9	488	5	ADI68789	Adi68789 Human ova	c 633	18	0.9	606	3	AAA16055	Aaa16055 Human col
561	18	0.9	488	10	ADH69125	Adh69125 Human tum	c 634	18	0.9	609	4	AAV09303	Abv09303 Human pro
562	18	0.9	490	4	AA191741	Aai91741 Human pol	c 635	18	0.9	609	4	AA524844	Aa524844 Human ova
563	18	0.9	491	12	ADQ20053	Adq20053 Human sof	c 636	18	0.9	609	5	AAH83481	Aah83481 Human ova
564	18	0.9	492	5	ADL40336	Adl40336 Human ova	c 637	18	0.9	609	10	ADC76399	Adc76399 DNA homol
565	18	0.9	494	5	AAH83612	Aah83612 Human ova	c 638	18	0.9	614	5	ADL36674	Adl36674 Human ova
566	18	0.9	497	5	ADI68714	Adi68714 Human ova	639	18	0.9	614	5	ADL171518	Adl171518 Human ova
567	18	0.9	497	5	ADI75075	Adi75075 Human ova	640	18	0.9	622	4	AA120340	Aa120340 Human bre
568	18	0.9	497	10	ADH69124	Adh69124 Human tum	c 641	18	0.9	622	4	AA524784	Aa524784 Human ova
569	18	0.9	498	5	ADI68770	Adi68770 Human ova	c 642	18	0.9	622	4	AA525232	Aa525232 Human ova
570	18	0.9	498	5	ADI75129	Adi75129 Human ova	c 643	18	0.9	622	5	AAH83418	Aah83418 Human ova
571	18	0.9	498	10	ADC93749	Adc93749 E. faecilu	c 644	18	0.9	622	5	AAH83418	Aah83418 Human ova
572	18	0.9	503	5	ABV60802	Abv60802 Human pro	c 645	18	0.9	623	6	ABT089450	Abt089450 Human pol
573	18	0.9	503	5	ADL40312	Adl40312 Human ova	c 646	18	0.9	624	6	ABT05956	Abt05956 Human pro
574	18	0.9	503	5	ADL40373	Adl40373 Human ova	647	18	0.9	625	5	ADL171284	Adl171284 Human ova
575	18	0.9	504	5	ADL40374	Adl40374 Human ova	648	18	0.9	625	5	ADL36444	Adl36444 Human ova
576	18	0.9	504	5	ADL39680	Adl39680 Human ova	649	18	0.9	629	5	ADL42828	Adl42828 Human bre
577	18	0.9	505	6	ABQ15474	Abq15474 Oligonuel	c 650	18	0.9	631	6	ABT11063	Abt11063 Human bre
578	18	0.9	505	6	AAH815475	Aah815475 Oligonuel	c 651	18	0.9	631	6	AA524766	Aa524766 Human ova
579	18	0.9	508	5	AAH83430	Aah83430 Human ova	c 652	18	0.9	635	4	AA525282	Aa525282 Human imm
580	18	0.9	510	6	ABQ30058	Abq30058 Oligonuel	c 653	18	0.9	635	5	AAH83399	Aah83399 Human ova
581	18	0.9	510	6	ABQ30059	Abq30059 Oligonuel	c 654	18	0.9	637	9	ACL15405	ACL15405 DNA clone
582	18	0.9	510	13	ACN45896	Acn45896 Cotton pr	655	18	0.9	637	9	ACL15405	ACL15405 DNA clone
583	18	0.9	511	5	ADL40384	Adl40384 Human ova	c 657	18	0.9	643	5	AAH83663	Aah83663 Human ova
584	18	0.9	513	5	ADL41858	Adl41858 Human ova	c 658	18	0.9	643	5	ADL41730	Adl41730 Human ova
585	18	0.9	514	5	AAH83810	Aah83810 Human ova	c 659	18	0.9	644	13	ACN54225	Acn54225 Cotton an
586	18	0.9	518	13	ACN61295	Acn61295 Cotton gy	660	18	0.9	650	5	AA521829	Aa521829 Human col
587	18	0.9	519	5	ADL36759	Adl36759 Human ova	661	18	0.9	651	5	ADL68806	Adl68806 Human ova
588	18	0.9	519	5	ADI71603	Adi71603 Human ova	662	18	0.9	651	5	ADL75165	Adi75165 Human ova
589	18	0.9	523	5	ADI75047	Adi75047 Human ova	c 663	18	0.9	658	10	ADC75131	Adc75131 Rice phyt
590	18	0.9	523	5	ADI68685	Adi68685 Human ova	c 664	18	0.9	658	10	ADK58531	Adk58531 Plant DNA
591	18	0.9	523	6	ABT05955	Abt05955 Human pro	c 666	18	0.9	666	5	ABV02117	Abv02117 Human pro
592	18	0.9	527	8	ABZ72991	Abz72991 Rice leaf	665	18	0.9	666	5	AAH18357	Aah18357 Human bre
593	18	0.9	531	5	ABV39452	Abv39452 Human pro	c 667	18	0.9	669	4	AA562889	Aa562889 Human G p
594	18	0.9	531	5	ABV45330	Abv45330 Human pro	668	18	0.9	677	6	AA562889	Aa562889 Human pro
595	18	0.9	531	5	ABV40866	Abv40866 Human pro	669	18	0.9	681	5	ABV22586	Abv22586 Human pro
596	18	0.9	531	5	ABV30479	Abv30479 Human pro	670	18	0.9	681	5	ABV21430	Abv21430 Human pro
597	18	0.9	531	5	ABV39429	Abv39429 Human pro	671	18	0.9	681	5	ABV23196	Abv23196 Human pro
598	18	0.9	533	13	ADQ51434	Adq51434 Novel can	672	18	0.9	681	5	ABV27248	Abv27248 Human pro
599	18	0.9	535	5	ADL39493	Adl39493 Human ova	673	18	0.9	681	5	ABV20129	Abv20129 Human pro
600	18	0.9	540	5	ABV58372	Abv58372 Human pro	674	18	0.9	681	5	ABV20144	Abv20144 Human pro
601	18	0.9	542	5	ADL40305	Adl40305 Human ova	675	18	0.9	681	5	ABV26835	Abv26835 Human pro
602	18	0.9	549	5	ADL39489	Adl39489 Human ova	676	18	0.9	681	5	ABV27156	Abv27156 Human pro
603	18	0.9	555	10	ABX05780	Abx05780 S. pneumo	677	18	0.9	681	5	ABV21337	Abv21337 Human pro
604	18	0.9	557	5	ABV32431	Abv32431 Human pro							

678	18	0.9	681	5	ABV29033	Abv29033 Human pro	c 751	18	0.9	1141	10	ADC87248	Adc87248 Human GPC
679	18	0.9	681	5	ABV23138	Abv23138 Human pro	c 752	18	0.9	1170	13	ADR73684	Adr73684 Rice prom
680	18	0.9	681	5	ABV25962	Abv25962 Human pro	c 753	18	0.9	1185	6	ABQ44170	Abq44170 Oligonucl
681	18	0.9	681	5	ABV22471	Abv22471 Human pro	c 754	18	0.9	1185	6	ABQ44171	Abq44171 Oligonucl
682	18	0.9	681	5	ABV24041	Abv24041 Human pro	c 755	18	0.9	1221	3	AAC47697	Aac47697 Arabidops
683	18	0.9	681	5	ABV28979	Abv28979 Human pro	c 756	18	0.9	1232	2	AZ16418	Aaz16418 Human gen
684	18	0.9	681	5	ABV28286	Abv28286 Human pro	c 757	18	0.9	1243	13	ADR73662	Adr73662 Rice prom
685	18	0.9	681	5	ABV28406	Abv28406 Human pro	c 758	18	0.9	1262	2	AAX84980	Aax84980 Human sec
686	18	0.9	681	5	ABV20989	Abv20989 Human pro	c 759	18	0.9	1262	8	ACD18906	Acd18906 Novel hum
687	18	0.9	681	5	ABV25977	Abv25977 Human pro	c 760	18	0.9	1262	12	ADG78297	Adg78297 Human sec
688	18	0.9	681	5	ADL45505	Adl45505 Human ova	c 761	18	0.9	1262	12	ADN60588	Adn60588 Human sec
689	18	0.9	684	3	AAO2603	Aao2603 Human col	c 762	18	0.9	1288	3	AAC34972	Aac34972 Arabidops
690	18	0.9	689	6	ABQ37596	Abq37596 Oligonucl	c 763	18	0.9	1318	6	AAS15009	Aas15009 Rice RecA
691	18	0.9	689	6	ABQ37597	Abq37597 Oligonucl	c 764	18	0.9	1358	12	ADQ25247	Adq25247 Human sof
692	18	0.9	702	5	ADL40401	Adl40401 Human ova	c 765	18	0.9	1358	12	ADQ25564	Adq25564 Human sof
693	18	0.9	705	5	ADL43058	Adl43058 Human ova	c 766	18	0.9	1416	8	ABZ35906	Abz35906 Human sec
694	18	0.9	705	6	ABQ34131	Abq34131 Oligonucl	c 767	18	0.9	1422	8	ABX72616	Abx72616 Human cdn
695	18	0.9	705	6	ABQ34130	Abq34130 Oligonucl	c 768	18	0.9	1428	3	AAC33787	Aac33787 Arabidops
696	18	0.9	706	6	ABQ43116	Abq43116 Oligonucl	c 769	18	0.9	1434	12	ADN10696	Adn10696 Nicotiana
697	18	0.9	706	6	ABQ43117	Abq43117 Oligonucl	c 770	18	0.9	1449	13	ADT47611	Adt47611 Bacterial
698	18	0.9	709	6	ABQ46435	Abq46435 Oligonucl	c 771	18	0.9	1464	8	ACA33146	Aca33146 Prokaryot
699	18	0.9	709	6	ABQ46434	Abq46434 Oligonucl	c 772	18	0.9	1485	10	ADH84460	Adh84460 Enterococ
700	18	0.9	711	4	ABL24699	Abi24699 Drosophil	c 773	18	0.9	1496	2	AAQ72271	Aaq72271 Rat MR77
701	18	0.9	714	4	ABL24699	Abi24699 Drosophil	c 774	18	0.9	1497	12	ADL16364	Adl16364 pBP118 ve
702	18	0.9	722	2	ADR02088	Adr02088 A. gossyp	c 775	18	0.9	1511	6	ABQ14697	Abq14697 Oligonucl
703	18	0.9	727	2	ADR02319	Adr02319 A. gossyp	c 776	18	0.9	1511	6	ABQ14696	Abq14696 Oligonucl
704	18	0.9	747	5	AS78273	Aas78273 DNA encod	c 777	18	0.9	1529	3	AAC54931	Aac54931 Arabidops
705	18	0.9	762	4	AA121674	Aai121674 Human bre	c 778	18	0.9	1537	3	AAC49912	Aac49912 Arabidops
706	18	0.9	794	5	ADL62414	Adl62414 Human ova	c 779	18	0.9	1539	3	AAC53145	Aac53145 Arabidops
707	18	0.9	803	4	AA526758	Aae26758 Human gen	c 780	18	0.9	1552	3	AAC40750	Aac40750 Arabidops
708	18	0.9	803	4	AA526761	Aae26761 Human gen	c 781	18	0.9	1576	5	AAF24154	Aaf24154 Human sec
709	18	0.9	803	8	ABX74110	Abx74110 Human nov	c 782	18	0.9	1589	12	ADH18972	Adh18972 Human cel
710	18	0.9	803	8	ABX74107	Abx74107 Human nov	c 783	18	0.9	1594	12	ADN10662	Adn10662 Nicotiana
711	18	0.9	816	13	ADR63888	Adr63888 Cotton cd	c 784	18	0.9	1601	12	ADN10704	Adn10704 Nicotiana
712	18	0.9	824	6	ABX91971	Abx91971 Lung spec	c 785	18	0.9	1605	2	AAZ00809	Aaz00809 Human sec
713	18	0.9	833	3	AAC49657	Aac49657 Arabidops	c 786	18	0.9	1610	12	ADN10642	Adn10642 Nicotiana
714	18	0.9	848	6	ABQ30456	Abq30456 Oligonucl	c 787	18	0.9	1623	12	ADN10600	Adn10600 Nicotiana
715	18	0.9	848	6	ABQ30457	Abq30457 Oligonucl	c 788	18	0.9	1636	6	ABN72979	Abn72979 Clone 077
716	18	0.9	850	6	ABQ48654	Abq48654 Oligonucl	c 789	18	0.9	1636	10	ADF08963	Adf08963 cDNA enco
717	18	0.9	850	6	ABQ48655	Abq48655 Oligonucl	c 790	18	0.9	1675	6	ABQ78825	Abq78825 Human Mch
718	18	0.9	852	4	AA561013	Aas61013 Human can	c 791	18	0.9	1679	6	AAL51168	Aal51168 Peroxidase
719	18	0.9	876	6	ABQ45452	Abq45452 Oligonucl	c 792	18	0.9	1679	6	AAL51168	Aal51168 Peroxidase
720	18	0.9	876	6	ABQ45453	Abq45453 Oligonucl	c 793	18	0.9	1704	3	AAC47127	Aac47127 Arabidops
721	18	0.9	878	6	ABQ35912	Abq35912 Oligonucl	c 794	18	0.9	1704	4	AD20618	Adc20618 Human ova
722	18	0.9	878	6	ABQ35913	Abq35913 Oligonucl	c 795	18	0.9	1721	12	ADH41325	Adh41325 Human ova
723	18	0.9	882	6	ABN91503	Abn91503 Staphyloc	c 796	18	0.9	1729	8	ACF62822	Acf62822 Colon can
724	18	0.9	882	13	ADS03045	Ads03045 Staphyloc	c 797	18	0.9	1761	3	AA70076	Aaa70076 Human ova
725	18	0.9	887	2	AAZ96455	Aaz96455 S. pneumo	c 798	18	0.9	1761	6	ABN72970	Abn72970 cDNA sequ
726	18	0.9	887	4	AA194177	Aai94177 Human neu	c 799	18	0.9	1761	9	ADA08540	Ada08540 Human ova
727	18	0.9	904	4	AA522326	Aae22326 Human cdn	c 800	18	0.9	1761	10	ADF08883	Adf08883 cDNA enco
728	18	0.9	935	4	AAU10399	Aai10399 Human bre	c 801	18	0.9	1761	10	ADG46170	Adg46170 Human ova
729	18	0.9	949	3	AAA35137	Aaa35137 Human ade	c 802	18	0.9	1767	2	AAX99572	Aax99572 Nucleic a
730	18	0.9	949	3	AAF21259	Aaf21259 Human low	c 803	18	0.9	1783	4	AAS34928	Aas34928 cDNA enco
731	18	0.9	949	10	ABZ96953	Abz96953 Human nuc	c 804	18	0.9	1783	10	ADC46086	Adc46086 Human neo
732	18	0.9	949	11	ABD20802	Abd20802 Human pul	c 805	18	0.9	1800	6	ABA04826	Abz04826 Human myo
733	18	0.9	971	11	ACN80598	Acn80598 Breast ca	c 806	18	0.9	1821	8	ACF73124	Acf73124 Staphyloc
734	18	0.9	972	13	ADC91448	Adc91448 E. faeciu	c 807	18	0.9	1845	6	AD343318	Adz43318 Human PKI
735	18	0.9	992	13	ADS47792	Ads47792 Bacterial	c 808	18	0.9	1893	6	ABN70106	Abn70106 Streptoco
736	18	0.9	1015	6	ABQ53075	Abq53075 Oligonucl	c 809	18	0.9	1941	6	ABQ54755	Abq54755 Human ova
737	18	0.9	1015	6	ABQ53074	Abq53074 Oligonucl	c 810	18	0.9	1981	3	AAX50482	Aax50482 Pain regu
738	18	0.9	1017	5	ABQ578120	Aab78120 DNA encod	c 811	18	0.9	1995	6	ABL88382	Abi88382 Pain regu
739	18	0.9	1019	13	ADR64356	Adr64356 Cotton cd	c 812	18	0.9	2000	6	ABZ15902	Abz15902 Arabidops
740	18	0.9	1049	6	ABQ29059	Abq29059 Oligonucl	c 813	18	0.9	2000	6	ABZ16643	Abz16643 Arabidops
741	18	0.9	1049	6	ABQ29058	Abq29058 Oligonucl	c 814	18	0.9	2000	6	ABZ15449	Abz15449 Arabidops
742	18	0.9	1049	12	ADO02565	Ado02565 Soybean o	c 815	18	0.9	2000	8	ADA72730	Ada72730 Rice gene
743	18	0.9	1049	13	ADI42014	Adi42014 Plant tra	c 816	18	0.9	2000	8	ADA72196	Ada72196 Rice gene
744	18	0.9	1059	10	ACF71850	Acf71850 Phororhab	c 817	18	0.9	2000	8	ADA71873	Ada71873 Rice gene
745	18	0.9	1060	6	ADN73046	Adn73046 cDNA sequ	c 818	18	0.9	2000	10	ACC60882	Acc60882 Gene sequ
746	18	0.9	1060	9	ADA08721	Ada08721 Human O77	c 819	18	0.9	2000	10	ADK62281	Adk62281 Disease t
747	18	0.9	1060	10	ADF09064	Adf09064 cDNA enco	c 820	18	0.9	2000	12	ADJ41413	Adj41413 Plant CDN
748	18	0.9	1071	5	AAC88100	Aac88100 Human FLE	c 821	18	0.9	2000	12	ADJ41180	Adj41180 Plant CDN
749	18	0.9	1074	3	AAZ52291	Aaz52291 Maize rep	c 822	18	0.9	2012	12	ADO21867	Ado21867 Human ves
750	18	0.9	1120	1	AAN70643	Aan70643 Cyclohexi	c 823	18	0.9	2017	2	AAT60713	Aat60713 Saccharom

824	18	0.9	2059	8	ABX95379	Abx95379 S. pneumoniae	897	18	0.9	2957	2	AAV18462	Aav18462 Human gra
825	18	0.9	2070	12	ADL16362	Adl16362 pBP116 ve	c 898	18	0.9	2957	5	AA592281	AA592281 DNA encod
c 826	18	0.9	2084	12	ADQ24447	Adq24447 Human sof	c 899	18	0.9	2996	3	AA70001	AA70001 Human ova
c 827	18	0.9	2090	11	ADI30900	Adi30900 Human cDN	900	18	0.9	2996	4	AAH55680	AAH55680 Human ova
c 828	18	0.9	2108	10	ADA52503	Ada52503 Human cod	901	18	0.9	2996	6	ABN72895	ABN72895 Full leng
c 829	18	0.9	2121	8	ABZ74640	Abz74640 Secreted	902	18	0.9	2996	6	ABN72974	ABN72974 Hypocheti
c 830	18	0.9	2121	8	ADA44569	Ada44569 Human sec	903	18	0.9	2996	9	ADA09060	Ada09060 Human ova
c 831	18	0.9	2121	12	ADN41709	Adn41709 Human sec	904	18	0.9	2996	9	ADA08615	Ada08615 Human O77
c 832	18	0.9	2122	8	ABZ74641	Abz74641 Secreted	905	18	0.9	2996	10	ADF08807	Adf08807 cDNA enco
c 833	18	0.9	2122	8	ADA44570	Ada44570 Human sec	906	18	0.9	2996	10	ADF08958	Adf08958 cDNA enco
c 834	18	0.9	2125	10	ACC72758	Acc72758 Human can	907	18	0.9	2996	10	ADA65555	Ada65555 Human ova
c 835	18	0.9	2136	10	ADH84180	Adh84180 Enterococ	908	18	0.9	2996	12	ADN40450	Adn40450 Human bre
c 836	18	0.9	2136	8	ABX63197	Abx63197 Human cDN	c 909	18	0.9	3002	4	ABL21972	ABL21972 Drosophil
c 837	18	0.9	2225	10	ADB62943	Adb62943 Human cDN	c 910	18	0.9	3007	13	ADR07533	ADR07533 Full leng
c 838	18	0.9	2284	4	ABL21228	AbL21228 Drosophil	c 911	18	0.9	3015	4	AAH54037	AAH54037 S. epider
c 839	18	0.9	2289	12	ADL16354	Adl16354 pBP109 ex	912	18	0.9	3060	4	AAF77098	AAf77098 Arabidops
c 840	18	0.9	2308	12	ADO21866	Ado21866 Human ves	913	18	0.9	3060	10	ACF35553	ACf35553 Arabidops
c 841	18	0.9	2314	6	ABK84154	Abk84154 Human cDN	914	18	0.9	3075	12	ADO35502	ADO35502 Novel mou
c 842	18	0.9	2318	3	AC559907	Ac559907 Human sec	915	18	0.9	3086	6	ABS66329	ABs66329 Soybean l
c 843	18	0.9	2318	8	ABZ73286	Abz73286 Secreted	c 916	18	0.9	3110	2	AA784234	AA784234 DNA encod
c 844	18	0.9	2318	10	ADC20067	Adc20067 Human sec	c 917	18	0.9	3114	6	ABS66336	ABs66336 Soybean l
c 845	18	0.9	2318	10	ABT16764	Abt16764 Human sec	c 918	18	0.9	3114	6	ABS66336	ABs66336 Soybean l
c 846	18	0.9	2318	10	ABZ66897	Abz66897 Human sec	c 919	18	0.9	3115	13	ADR23587	ADR23587 Breast ca
c 847	18	0.9	2319	10	ADI57341	Adi57341 Human cel	c 920	18	0.9	3157	4	AA536928	AA536928 Human car
c 848	18	0.9	2323	13	ADT66713	Adt66713 Human CDC	c 921	18	0.9	3157	13	ADJ09040	ADj09040 Human car
c 849	18	0.9	2337	12	ADL16340	Adl16340 Bacillus	c 922	18	0.9	3157	10	AA536929	AA536929 Human car
c 850	18	0.9	2344	5	AA566472	AA566472 DNA encod	c 923	18	0.9	3169	10	ADE47622	ADe47622 Human car
c 851	18	0.9	2396	10	ACF58208	ACf58208 B. anthrac	c 924	18	0.9	3169	10	ADE47623	ADe47623 Human car
c 852	18	0.9	2415	4	AAI98104	AAi98104 Human neu	c 925	18	0.9	3176	13	ADJ09041	ADj09041 Human car
c 853	18	0.9	2422	6	AAI97665	AAi97665 Human G-P	c 926	18	0.9	3176	3	AA76094	AA76094 Human ORF
c 854	18	0.9	2430	4	AA56015	AA56015 Wild type	c 927	18	0.9	3188	6	ABL61777	ABl61777 Colon ade
c 855	18	0.9	2449	11	ADM01613	Adm01613 Human cDN	c 928	18	0.9	3188	9	ACC85162	ACC85162 Human P13
c 856	18	0.9	2481	4	AAH26415	AAh26415 Arancicola	c 929	18	0.9	3188	10	ADD29777	ADD29777 Human tum
c 857	18	0.9	2481	9	ADA09915	Ada09915 Human rec	c 930	18	0.9	3190	2	AA211494	AA211494 Human pro
c 858	18	0.9	2489	2	AAZ31960	AAz31960 S. pneumo	c 931	18	0.9	3201	12	ADO35413	ADO35413 Novel mou
c 859	18	0.9	2512	4	ABL22466	ABl22466 Drosophil	c 932	18	0.9	3222	8	ABX95377	ABx95377 DNA encod
c 860	18	0.9	2533	2	AAI13589	AAi13589 Enterococ	c 933	18	0.9	3294	2	AAQ70179	AAq70179 Sequence
c 861	18	0.9	2533	6	ABS99384	ABs99384 Enterococ	c 934	18	0.9	3298	5	ABV25485	ABv25485 Human pro
c 862	18	0.9	2537	4	ABL21768	ABl21768 Drosophil	c 935	18	0.9	3323	4	ABL15666	ABl15666 Drosophil
c 863	18	0.9	2544	4	ABL09232	ABl09232 Drosophil	c 936	18	0.9	3400	2	AAI02979	AAi02979 Human IL-
c 864	18	0.9	2560	6	ABN59748	ABn59748 Novel hum	c 937	18	0.9	3418	4	ABL02858	ABl02858 Drosophil
c 865	18	0.9	2574	11	ADM01989	Adm01989 Human cDN	c 938	18	0.9	3447	6	ABN72972	ABn72972 Truncated
c 866	18	0.9	2608	3	AA770075	AA770075 Human ova	c 939	18	0.9	3447	9	ADA08609	Ada08609 Human O77
c 867	18	0.9	2608	3	ABN72969	ABn72969 cDNA sequ	c 940	18	0.9	3447	10	ADF08952	ADF08952 cDNA enco
c 868	18	0.9	2608	9	ADA08539	Ada08539 Human ova	c 941	18	0.9	3447	10	ADG46239	ADg46239 Human ova
c 869	18	0.9	2608	10	ADF08882	Adf08882 cDNA enco	c 942	18	0.9	3463	2	AA761728	AA761728 Streptoco
c 870	18	0.9	2608	10	ADG46169	ADg46169 Human ova	c 943	18	0.9	3463	2	AA761728	AA761728 Streptoco
c 871	18	0.9	2611	6	ABZ70189	Abz70189 Ribosomal	c 944	18	0.9	3467	13	ADR06673	ADR06673 Full leng
c 872	18	0.9	2622	4	ABK42633	ABk42633 Genomic s	c 945	18	0.9	3521	10	ADE61538	ADe61538 Human gen
c 873	18	0.9	2622	5	ABA20094	ABa20094 Human ner	c 946	18	0.9	3529	4	ABL05022	ABl05022 Drosophil
c 874	18	0.9	2622	9	ADB60789	Adb60789 Connectiv	c 947	18	0.9	3529	4	ABL05022	ABl05022 Drosophil
c 875	18	0.9	2638	4	AAC84370	AAc84370 Mouse Zac	c 948	18	0.9	3546	8	ABX05223	ABx05223 Human nov
c 876	18	0.9	2638	10	ABX93337	ABx93337 cDNA enco	c 949	18	0.9	3557	4	AAH18639	AAh18639 Human cDN
c 877	18	0.9	2686	2	AAV82467	AAv82467 Recombina	c 950	18	0.9	3557	5	ABN72973	ABn72973 Full nucl
c 878	18	0.9	2703	4	ABL11944	ABl11944 Drosophil	c 951	18	0.9	3557	6	ABN72975	ABn72975 cDNA sequ
c 879	18	0.9	2720	12	ADQ24606	Adq24606 Human sof	c 952	18	0.9	3557	9	ADA08610	Ada08610 Human O77
c 880	18	0.9	2720	12	ADQ24903	Adq24903 Human sof	c 953	18	0.9	3557	9	ADA08616	Ada08616 Human cDN
c 881	18	0.9	2779	4	ABL24698	ABl24698 Drosophil	c 954	18	0.9	3557	10	ADF08953	ADF08953 cDNA enco
c 882	18	0.9	2796	2	AAV82472	AAv82472 Recombina	c 955	18	0.9	3557	10	ADF08959	ADF08959 cDNA enco
c 883	18	0.9	2800	4	ABL22214	ABl22214 Drosophil	c 956	18	0.9	3557	10	ADG46240	ADg46240 Human ova
c 884	18	0.9	2851	13	ADR08132	ADR08132 Full leng	c 957	18	0.9	3557	12	ADQ08770	ADq08770 Human ova
c 885	18	0.9	2901	4	AAH54046	AAh54046 S. epider	c 958	18	0.9	3557	12	ADQ29638	ADq29638 Human col
c 886	18	0.9	2903	5	AA578152	AA578152 DNA encod	c 959	18	0.9	3574	10	ADD25507	ADD25507 Binding d
c 887	18	0.9	2932	8	ABZ10173	ABz10173 Haematopo	c 960	18	0.9	3576	4	ABL41162	ABl41162 Drosophil
c 888	18	0.9	2932	10	ADB54205	ADB54205 Pretreate	c 961	18	0.9	3596	4	ABL27422	ABl27422 Drosophil
c 889	18	0.9	2932	10	ADB84141	ADB84141 Human lym	c 962	18	0.9	3596	4	ABL27422	ABl27422 Drosophil
c 890	18	0.9	2932	13	ADS89505	ADs89505 Oligonuel	c 963	18	0.9	3600	11	ACN91879	ACn91879 Breast ca
c 891	18	0.9	2943	3	AA700074	AA700074 Human ova	c 964	18	0.9	3600	11	ACN91879	ACn91879 Breast ca
c 892	18	0.9	2943	6	ABN72968	ABn72968 cDNA sequ	c 965	18	0.9	3613	13	ADR08401	ADR08401 Full leng
c 893	18	0.9	2943	10	ADA08538	Ada08538 Human ova	c 966	18	0.9	3631	12	ADL72876	ADl72876 Anthrax v
c 894	18	0.9	2943	9	ADF08881	Adf08881 cDNA enco	c 967	18	0.9	3631	12	ADL72876	ADl72876 Anthrax v
c 895	18	0.9	2943	10	ADG46168	ADg46168 Human ova	c 968	18	0.9	3694	4	ABL21736	ABl21736 Drosophil
c 896	18	0.9	2949	4	ABL23052	ABl23052 Drosophil	c 969	18	0.9	3720	6	AAAD27687	AAAd27687 Plasmid p
										3732	4	ABL03714	ABl03714 Drosophil

c 970	18	0.9	3732	4	ABL20934
c 971	18	0.9	3738	12	ADQ24115
c 972	18	0.9	3743	12	ADQ64985
c 973	18	0.9	3798	10	ABX08985
974	18	0.9	3800	2	AAX28141
975	18	0.9	3800	3	AAZ60808
976	18	0.9	3835	4	AAH54069
c 977	18	0.9	3892	7	ADR41249
c 978	18	0.9	3901	13	ADR06677
979	18	0.9	3914	12	ADQ08599
980	18	0.9	3929	3	AAA34950
981	18	0.9	3929	3	AAF21072
982	18	0.9	3929	10	ABZ96766
983	18	0.9	3929	11	ABD20615
984	18	0.9	3983	1	AAN90569
985	18	0.9	3993	4	AAH54621
986	18	0.9	4001	13	ADS89768
c 987	18	0.9	4083	5	AAS83954
988	18	0.9	4110	8	ABZ10055
c 989	18	0.9	4148	6	ABK64835
c 990	18	0.9	4148	10	ADF09649
c 991	18	0.9	4148	13	ACN37699
992	18	0.9	4184	13	ADR08234
c 993	18	0.9	4209	5	ADL62845
c 994	18	0.9	4224	13	ADS46785
c 995	18	0.9	4253	3	AAF18289
996	18	0.9	4305	8	ACA52686
c 997	18	0.9	4453	4	ABL09288
998	18	0.9	4458	4	AAK69549
999	18	0.9	4494	12	ADH41327
c1000	18	0.9	4497	4	AAF55367

ALIGNMENTS

RESULT 1
ABZ75215
ID ABZ75215 standard; cDNA; 2030 BP.

AC ABZ75215;
DT 23-APR-2003 (first entry)
XX Arabidopsis thaliana endomembrane associated promoter cDNA.
DE Arabidopsis thaliana endomembrane associated; promoter; expression; gene; ss.
XX ENDO; endomembrane associated; promoter; expression; gene; ss.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX WO200268665-A2.

XX 06-SEP-2002.

XX 14-FEB-2002; 2002WO-EP002894.

XX 22-FEB-2001; 2001US-0270779P.

XX (RHOB-) RHOBIO.

XX Thomas T, Nuccio M, Hsieh T;

XX WPI; 2002-707007/76.

XX New isolated ENDO promoter from the gene of Arabidopsis thaliana, useful

XX for directing expression of genes in plants.

XX Claim 1; Page 17; 18pp; English.

XX The invention relates to the novel isolated Arabidopsis thaliana
CC endomembrane associated (ENDO) gene promoter sequence. The nucleic acid
CC is useful for directing expression of genes in plants. The present
CC sequence represents the A. thaliana ENDO promoter of the invention

XX	Sequence	2030 BP;	722 A;	287 C;	319 G;	702 T;	0 U;	0 Other;
SQ	Query Match	100.0%;	Score	2030;	DB	6;	Length	2030;
	Best Local Similarity	100.0%;	Pred.	No.	0;			
	Matches	2030;	Conservative	0;	Mismatches	0;	Indels	0;
	Gaps	0;						
QY	1	CTTCATAGAAGGATGGACCATTTGAAGATACCTTTCTCTCTTTCTATTTTATTTGATTTAG	60					
DB	1	CTTCATAGAAGGATGGACCATTTGAAGATACCTTTCTCTCTTTCTATTTTATTTGATTTAG	60					
QY	61	AAATCATATTCATTACAAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTTATAAC	120					
DB	61	AAATCATATTCATTACAAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTTATAAC	120					
QY	121	TTACAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGG	180					
DB	121	TTACAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGG	180					
QY	181	TTTAGGAAAAATGTATCTTTTCATATATAAATAATATAGATCTTCAAGAAGCTGAATT	240					
DB	181	TTTAGGAAAAATGTATCTTTTCATATATAAATAATATAGATCTTCAAGAAGCTGAATT	240					
QY	241	GGGTTTCCAACTATTTTATCGTTTGACACTACTTTGACTTATCAAAAAGAGTTCAAAATA	300					
DB	241	GGGTTTCCAACTATTTTATCGTTTGACACTACTTTGACTTATCAAAAAGAGTTCAAAATA	300					
QY	301	GAATAATAGAATCGAATCACAGTTTTCAGTTGAAGAGGATTTGATATTTGGTCGACATTT	360					
DB	301	GAATAATAGAATCGAATCACAGTTTTCAGTTGAAGAGGATTTGATATTTGGTCGACATTT	360					
QY	361	TAAAGAGTTGTTGTTTTCATCTGCAATCTGCGTGGTTTTCGTTCCGTTGAACCAAT	420					
DB	361	TAAAGAGTTGTTGTTTTCATCTGCAATCTGCGTGGTTTTCGTTCCGTTGAACCAAT	420					
QY	421	TCAACACTTTGTATAAACCAGTAATAGTATATACTAGACGTACGCCAATACCAAAATAAA	480					
DB	421	TCAACACTTTGTATAAACCAGTAATAGTATATACTAGACGTACGCCAATACCAAAATAAA	480					
QY	481	ATTAATACTCAATTCACAAATTTGAATCTACACCATATCATGCAATATATACGCAACCTA	540					
DB	481	ATTAATACTCAATTCACAAATTTGAATCTACACCATATCATGCAATATATACGCAACCTA	540					
QY	541	GAATAATCAATGAAATTTAATCGAGGATAATCAATATCCAACTCAACGATATCAAAAGC	600					
DB	541	GAATAATCAATGAAATTTAATCGAGGATAATCAATATCCAACTCAACGATATCAAAAGC	600					
QY	601	CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTAATATACATTTGTTGTTA	660					
DB	601	CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTAATATACATTTGTTGTTA	660					
QY	661	AACAGATAATATACATTTAATAGTATGAAATAGTAATAGTAATAGTAATAGAGAGCGTA	720					
DB	661	AACAGATAATATACATTTAATAGTATGAAATAGTAATAGTAATAGTAATAGAGAGCGTA	720					
QY	721	TATGTTTACAACCTACAGATCACCATCCCAATTAACAATCCGATTCGTGGGCCCAATGTT	780					
DB	721	TATGTTTACAACCTACAGATCACCATCCCAATTAACAATCCGATTCGTGGGCCCAATGTT	780					
QY	781	TCGATATTTGGCAACTGTGATTGATGTGACTGCCAGCTGGCATATTTTCCCTCTCGATT	840					
DB	781	TCGATATTTGGCAACTGTGATTGATGTGACTGCCAGCTGGCATATTTTCCCTCTCGATT	840					
QY	841	ACGTTTTTACCGTTTCCCTCTCTGTTTCCAGGTTAAATTTCAATTTTACTATTGTACCGCT	900					
DB	841	ACGTTTTTACCGTTTCCCTCTCTGTTTCCAGGTTAAATTTCAATTTTACTATTGTACCGCT	900					
QY	901	GTCTTTTCACTTTTAAAGAAAAACCCAACTAATACTATACCGAATACATCTG	960					
DB	901	GTCTTTTCACTTTTAAAGAAAAACCCAACTAATACTATACCGAATACATCTG	960					
QY	961	CTTCATGTTGAGCTAACAGACTTATTTTCCGGTTGAAATTTGGTTTAACTTATCGATT	1020					
DB	961	CTTCATGTTGAGCTAACAGACTTATTTTCCGGTTGAAATTTGGTTTAACTTATCGATT	1020					

Db 961 CTTCTAGTGACGTAACAAGACTTATTTTCCGGTTGAAATTTGGTTAACTATTGAGATT 1020
Qy 1021 GTGCTAACCGAAAAACAGAACGGTTATGACGCCAACAGAGCGGAGGGGTAAAAACGAGAA 1080
Db 1021 GTGCTAACCGAAAAACAGAACGGTTATGACGCCAACAGAGCGGAGGGGTAAAAACGAGAA 1080
Qy 1081 AGAGGGGATGGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGTTCACGATAAGTC 1140
Db 1081 AGAGGGGATGGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGTTCACGATAAGTC 1140
Qy 1141 TGTCTATATGACGCGAAAGGGTTTCTTAAATTCAGAGACAATTAATCAGTTTCGTGTG 1200
Db 1141 TGTCTATATGACGCGAAAGGGTTTCTTAAATTCAGAGACAATTAATCAGTTTCGTGTG 1200
Qy 1201 TTTGGAGAAGAAGAACAGATCAATATACGAGGAGAGATCTCTAAGAGATTTATCGTT 1260
Db 1201 TTTGGAGAAGAAGAACAGATCAATATACGAGGAGAGATCTCTAAGAGATTTATCGTT 1260
Qy 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACACGTCGTG 1320
Db 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACACGTCGTG 1320
Qy 1321 TCTTCGTTTCGATTCCTAGATACGATTTTCTAGTTCATGTGAATGAATCTCTGTTTATTAC 1380
Db 1321 TCTTCGTTTCGATTCCTAGATACGATTTTCTAGTTCATGTGAATGAATCTCTGTTTATTAC 1380
Qy 1381 TACTAGGTTGTTCAATATATTTTCCGAGAAATTAACGAGAGAACAAAGTTAGTGAATATAT 1440
Db 1381 TACTAGGTTGTTCAATATATTTTCCGAGAAATTAACGAGAGAACAAAGTTAGTGAATATAT 1440
Qy 1441 TGAATCAGAGATGAAGATTAATATATACATAAATCATGTTTCTCTCAAGCATCTACGT 1500
Db 1441 TGAATCAGAGATGAAGATTAATATATACATAAATCATGTTTCTCTCAAGCATCTACGT 1500
Qy 1501 TGAATATATATAAAGAGTTTCTTTTGGTGAAAAAATATGTATGAGAAGTTTCATCTTC 1560
Db 1501 TGAATATATATAAAGAGTTTCTTTTGGTGAAAAAATATGTATGAGAAGTTTCATCTTC 1560
Qy 1561 ATAATAGTGAACAACCTCTCTTCATACCAAAAAAATTTGAAAAAATTTAGTGAAA 1620
Db 1561 ATAATAGTGAACAACCTCTCTTCATACCAAAAAAATTTGAAAAAATTTAGTGAAA 1620
Qy 1621 CTCTCTTCTGCGAATAGGTAGTTGGTTCAGATCAAAATACGATTAGCATAACAA 1680
Db 1621 CTCTCTTCTGCGAATAGGTAGTTGGTTCAGATCAAAATACGATTAGCATAACAA 1680
Qy 1681 ATTTTGTGCGATGCGCAATATTTCTGTCAGGTAAAAATATACCAATAGAAAAATATTTTA 1740
Db 1681 ATTTTGTGCGATGCGCAATATTTCTGTCAGGTAAAAATATACCAATAGAAAAATATTTTA 1740
Qy 1741 GGAGTATGATTAAGATTATGATGAAGAAATCTATTACGATAAGCAATAAATTTTCTTTTG 1800
Db 1741 GGAGTATGATTAAGATTATGATGAAGAAATCTATTACGATAAGCAATAAATTTTCTTTTG 1800
Qy 1801 CTGTTCTTGGTTTTTGTGCTTTTATAGAAATGATGATGCTTTTGTGTTTTTTCACC 1860
Db 1801 CTGTTCTTGGTTTTTGTGCTTTTATAGAAATGATGATGCTTTTGTGTTTTTTCACC 1860
Qy 1861 AGTAGATGCTACTATACACATAAGTAAACATGGGTAGTTTATATATAGAGAGATTGA 1920
Db 1861 AGTAGATGCTACTATACACATAAGTAAACATGGGTAGTTTATATATAGAGAGATTGA 1920
Qy 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAAATATGCTGTAATAATTTATGTTTATTAATTT 1980
Db 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAAATATGCTGTAATAATTTATGTTTATTAATTT 1980
Qy 1981 GACAGATTGTTTACGTTGAGAAGTTTAAATTTAGATTAAACACAAAAAG 2030
Db 1981 GACAGATTGTTTACGTTGAGAAGTTTAAATTTAGATTAAACACAAAAAG 2030

ID ABZ75216 standard; cDNA; 2042 BP.
XX
AC ABZ75216;
XX
DT 23-APR-2003 (first entry)
XX
DE Arabidopsis thaliana RC15 clone promoter fragment cDNA.
XX
KW ENDO; endomembrane associated; promoter; expression; gene; RC15; ss.
XX
OS Arabidopsis thaliana.
OS Synthetic.
PN W0200268665-A2.
XX
PD 06-SEP-2002.
XX
PF 14-FEB-2002; 2002WO-EP002894.
XX
PR 22-FEB-2001; 2001US-0270779P.
XX
PA (RHOB-) RHOBIO.
XX
PI Thomas T, Nuccio M, Heieh T;
XX
DR WPI; 2002-707007/76.
XX
PT New isolated ENDO promoter from the gene of Arabidopsis thaliana, useful
for directing expression of genes in plants.
XX
PS Example 1; Page 18; 18pp; English.
XX
CC The invention relates to the novel isolated Arabidopsis thaliana
endomembrane associated (ENDO) gene promoter sequence. The nucleic acid
is useful for directing expression of genes in plants. The present
sequence represents the promoter fragment taken from A. thaliana clone
RC15
XX
SQ Sequence 2042 BP; 725 A; 290 C; 322 G; 705 T; 0 U; 0 Other;
Query Match 100.0%; Score 2030; DB 6; Length 2042;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTCTAGAGAGGTGACCATTCGAAGAATACCTTCTCTTTCTATTATTTTATTGATTAG 60
Db 7 CTTCTAGAGAGGTGACCATTCGAAGAATACCTTCTCTTTCTATTATTTTATTGATTAG 66
Qy 61 AAAATCATATTTCAATTACAAAAGGAAAAAATAATTTTCTATCTCTAAAGTTATAAC 120
Db 67 AAAATCATATTTCAATTACAAAAGGAAAAAATAATTTTCTATCTCTAAAGTTATAAC 126
Qy 121 TTACAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTGG 180
Db 127 TTACAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTGG 186
Qy 181 TTTTGGAAAAATGATCTTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATT 240
Db 187 TTTTGGAAAAATGATCTTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATT 246
Qy 241 GGGTTTTCACACTATTTTATCGTTTTCAGCTACTTTGACTTTATCAAAGAGTTCAAAATA 300
Db 247 GGGTTTTCACACTATTTTATCGTTTTCAGCTACTTTGACTTTATCAAAGAGTTCAAAATA 306
Qy 301 GAAAAATAGAAATCGAATCAACACGTTTTCAGTGTGAAGGGATTTGATATTGGTGCACATTT 360
Db 307 GAAAAATAGAAATCGAATCAACACGTTTTCAGTGTGAAGGGATTTGATATTGGTGCACATTT 366
Qy 361 TAAAGAGTTGTTTTGTTTTTTTTTTTCCAACTCGATGTTTTTTCGTTCCGTTGAACCAAT 420
Db 367 TAAAGAGTTGTTTTGTTTTTTTTTTTCCAACTCGATGTTTTTTCGTTCCGTTGAACCAAT 426
Qy 421 TCAACACTTTGTATAAAAACCGAATAGTAAATATATAGTAGACGTACGCCAATACCAAAAAATAA 480

[illegible]

Db	1507	TGAATATATATAGAAGTTTTTTTTTTTGGTGAAAAAATATGTATGAGAAAGTTCAATCTTTC	1561
Qy	1561	ATAATAGTGAACAACTCTCTTTTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAA	1620
Db	1567	ATAATAGTGAACAACTCTCTTTTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAA	1626
Qy	1621	CTCTCTTTGTCGGAATAGGTTAGGTTTGGACTCAGAAATCAAAATACGATTAGCATAACAA	1680
Db	1627	CTCTCTTTGTCGGAATAGGTTAGGTTTGGACTCAGAAATCAAAATACGATTAGCATAACAA	1686
Qy	1681	ATTTTTTGGCATGGCAATTAATCTCTCGAGTAAATATACCAATAGAAAACATATTTTTTA	1740
Db	1687	ATTTTTTGGCATGGCAATTAATCTCTCGAGTAAATATACCAATAGAAAACATATTTTTTA	1746
Qy	1741	GGAGTAGTTAAGATTATGATTGAAGAAATACTATTACGATAAGCATAAAAATTTTCTTTTG	1800
Db	1747	GGAGTAGTTAAGATTATGATTGAAGAAATACTATTACGATAAGCATAAAAATTTTCTTTTG	1806
Qy	1801	CTGTTCTTGTTTTGTCGTTTTTATAGAACATTCGAAATATGCTATTTGTTTTTTTTTTCACC	1860
Db	1807	CTGTTCTTGTTTTGTCGTTTTTATAGAACATTCGAAATATGCTATTTGTTTTTTTTTTCACC	1866
Qy	1861	AGTAGATATGTACTATACACATACGATTAAGTACATGGGTAGTTTATATAGAGAGAGATTGA	1920
Db	1867	AGTAGATATGTACTATACACATACGATTAAGTACATGGGTAGTTTATATAGAGAGAGATTGA	1926
Qy	1921	TTTTTTCGTATATTTCTTTTGTGAAAAATAATATGTGTAAAAATTTATTGTTTATTAATTT	1980
Db	1927	TTTTTTCGTATATTTCTTTTGTGAAAAATAATATGTGTAAAAATTTATTGTTTATTAATTT	1986
Qy	1981	GACAGATTGTTCTACGTTGAGAAAGTTTAAATTTAGATTAAACAACAAAAAAG 2030	
Db	1987	GACAGATTGTTCTACGTTGAGAAAGTTTAAATTTAGATTAAACAACAAAAAAG 2036	
RESULT 3			
ABZ16347			
ID	ABZ16347	standard; DNA; 1064 BP.	
XX	XX	ABZ16347;	
AC	XX		
DT	XX	21-JAN-2003 (first entry)	
DE	XX	Arabidopsis thaliana stress regulated gene SEQ ID NO 4152.	
KW	XX	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	
OS	XX	Arabidopsis thaliana.	
PN	XX	WO200216655-A2.	
XX	XX	28-FEB-2002.	
PF	XX	24-AUG-2001; 2001WO-US026685.	
PR	XX	24-AUG-2000; 2000US-0227866P.	
PR	XX	26-JAN-2001; 2001US-0264647P.	
PR	XX	22-JUN-2001; 2001US-0300111P.	
XX	XX	(SCRI) SCRIPPS RES INST.	
PA	XX	(SYGN) SYNGENTA PARTICIPATIONS AG.	
PI	XX	Harper JF, Kreps J, Wang X, Zhu T;	
XX	XX	WPI; 2002-304127/34.	
XX	XX	Identifying a stress condition to which a plant cell has been exposed and	
PT	XX	producing plants with increased tolerance to these abiotic stresses.	
PS	XX	Claim 144; SEQ ID NO 4152; 577pp + Sequence Listing; English.	
CC	XX	The invention relates to identifying a stress condition to which a plant	
CC	XX	cell has been exposed, comprising: (a) contacting nucleic acid	

PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 18-AUG-1999; 99US-0149426P.
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PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
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PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.5%; Score 91; DB 3; Length 999;
Best Local Similarity 100.0%; Pred. No. 4.6e-30; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1174 AGAGAGACAATAATCAGTTTCGTGTTGGAGAGAAGACAGATCAAATACGAG 1233
DB 1 AGAGAGACAATAATCAGTTTCGTGTTGGAGAGAAGACAGATCAAATACGAG 60
QY 1234 GAGAGATCTCTAAGAGATTATCGTTTCAA 1264
DB 61 GAGAGATCTCTAAGAGATTATCGTTTCAA 91

RESULT 5
AAC37034
ID AAC37034 standard; DNA; 1001 BP.
XX
AC AAC37034;
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15944.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD
XX 06-SEP-2000.
PF
XX 25-FEB-2000; 2000EP-00301439.
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 25-MAR-1999; 99US-0126264P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.

PR	06-AUG-1999;	99US-0147303P.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
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PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139464P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139465P.	PR	27-AUG-1999;	99US-0151066P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151068P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151080P.
PR	21-JUN-1999;	99US-0139817P.	PR	30-AUG-1999;	99US-0151303P.
PR	22-JUN-1999;	99US-0139899P.	PR	31-AUG-1999;	99US-0151438P.
PR	23-JUN-1999;	99US-0140353P.	PR	01-SEP-1999;	99US-0151930P.
PR	23-JUN-1999;	99US-0140354P.	PR	07-SEP-1999;	99US-0152363P.
PR	24-JUN-1999;	99US-0140695P.	PR	10-SEP-1999;	99US-0153070P.
PR	28-JUN-1999;	99US-0140823P.	PR	13-SEP-1999;	99US-0153758P.
PR	28-JUN-1999;	99US-0140991P.	PR	15-SEP-1999;	99US-0154018P.
PR	30-JUN-1999;	99US-0141287P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0141842P.	PR	20-SEP-1999;	99US-0154779P.
PR	01-JUL-1999;	99US-0142154P.	PR	22-SEP-1999;	99US-0155139P.
PR	02-JUL-1999;	99US-0142055P.	PR	23-SEP-1999;	99US-0155486P.
PR	06-JUL-1999;	99US-0142390P.	PR	24-SEP-1999;	99US-0155659P.
PR	08-JUL-1999;	99US-0142803P.	PR	28-SEP-1999;	99US-0156458P.
PR	08-JUL-1999;	99US-0142920P.	PR	29-SEP-1999;	99US-0156596P.
PR	12-JUL-1999;	99US-0142977P.	PR	04-OCT-1999;	99US-0157117P.
PR	13-JUL-1999;	99US-0143542P.	PR	05-OCT-1999;	99US-0157753P.
PR	14-JUL-1999;	99US-0143624P.	PR	06-OCT-1999;	99US-0157865P.
PR	15-JUL-1999;	99US-0144005P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144085P.	PR	08-OCT-1999;	99US-0158232P.
PR	16-JUL-1999;	99US-0144086P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144325P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144333P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159330P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144332P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159638P.
PR	20-JUL-1999;	99US-0144884P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160815P.
PR	22-JUL-1999;	99US-0145192P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160989P.
PR	23-JUL-1999;	99US-0145224P.	PR	25-OCT-1999;	99US-0161404P.
PR	23-JUL-1999;	99US-0145224P.	PR	25-OCT-1999;	99US-0161405P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145913P.	PR	26-OCT-1999;	99US-0161359P.
PR	27-JUL-1999;	99US-0145918P.	PR	26-OCT-1999;	99US-0161360P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161361P.
PR	28-JUL-1999;	99US-0145951P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146386P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.			
PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.			

CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful for
CC enhancing or inhibiting production of a biosynthetic product in a plant.
CC (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=999909770445

XX Sequence 1088 BP; 270 A; 264 C; 179 G; 375 T; 0 U; 0 Other;

Query Match 2.6%; Score 53; DB 6; Length 1088;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 AGAAGAACAGATCAAAATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAA 1264
|||||
DB 1066 AGAAGAACAGATCAAAATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAA 1014

RESULT 9

ADM03675/c
ID ADM03675 standard; cDNA; 2550 BP.

XX ADM03675;

XX 20-MAY-2004 (first entry)

XX Human cDNA of the invention SEQ ID NO:2360.

XX ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hito Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-723558/69.

DR P-PSDB; ADM06118.

XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 2360; 305pp; English.

CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.

XX Sequence 2550 BP; 729 A; 546 C; 616 G; 659 T; 0 U; 0 Other;

Query Match 1.1%; Score 23; DB 11; Length 2550;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1928 TATATTCTTTTGTGAAAATAA 1950
|||||
DB 1783 TATATTCTTTTGTGAAAATAA 1761

RESULT 10

ABL98998

ID ABL98998 standard; cDNA; 427 BP.

XX ABL98998;

XX 25-JUN-2002 (first entry)

XX Mouse neuronal regeneration related polynucleotide SEQ ID NO 42.

XX Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
KW learning disorder; serial analysis of gene expression; SAGE;
KW gene expression; hippocampus; ss.

XX Mus sp.

XX DE10048893-A1.

XX 11-APR-2002.

XX 02-OCT-2000; 2000DE-01048893.

XX 02-OCT-2000; 2000DE-01048893.

XX (LION-) LION BIOSCIENCE AG.

XX WPI; 2002-341428/38.

XX New nucleic acids involved in neuronal regeneration, useful in screening
PT for modulators of regeneration or synaptic efficiency, and potential
PT therapeutic agents.

XX Claim 5; Page 27; 38pp; German.

XX The invention relates to nucleic acids (ABL98957-ABL99004) involved in
CC regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)
CC used to screen for compounds and potential therapeutic agents that
CC modulate nerve cell regeneration and/or synaptic efficiency. They may
CC also be used for treatment or diagnosis of defective or pathological
CC memory and learning conditions

XX Sequence 427 BP; 116 A; 85 C; 96 G; 130 T; 0 U; 0 Other;

Query Match 1.1%; Score 22; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAATTTGAAAAAAA 1611
|||||
DB 8 AAAAAAATTTGAAAAAAA 29

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RESULT 11
ABL98999/c
ID ABL98999 standard; cDNA; 427 BP.
XX AC ABL98999;
XX AC ABL98999;
XX DT 25-JUN-2002 (first entry)
XX DE Mouse neuronal regeneration related polynucleotide SEQ ID NO 43.
XX DE Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
XX KW learning disorder; serial analysis of gene expression; SAGE;
XX KW gene expression; hippocampus; ss.
XX OS Mus sp.
XX PN DE1004893-A1.
XX PD 11-APR-2002.
XX PF 02-OCT-2000; 2000DE-01048893.
XX PR 02-OCT-2000; 2000DE-01048893.
XX PA (LION-) LION BIOSCIENCE AG.
XX DR WPI; 2002-341428/38.
XX PT New nucleic acids involved in neuronal regeneration, useful in screening
XX PT for modulators of regeneration or synaptic efficiency, and potential
XX PT therapeutic agents.
XX PS Claim 5; Page 27; 38pp; German.
XX CC The invention relates to nucleic acids (ABL98997-ABL99004) involved in
XX CC regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)
XX CC used to screen for compounds and potential therapeutic agents that
XX CC modulate nerve cell regeneration and/or synaptic efficiency. They may
XX CC also be used for treatment or diagnosis of defective or pathological
XX CC memory and learning conditions
XX CC
XX SQ Sequence 427 BP; 130 A; 96 C; 85 G; 116 T; 0 U; 0 Other;

Query Match 1.1%; Score 22; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAAAAATTTGAAAAAAAAA 1611
Db 420 AAAAAAAAAATTTGAAAAAAAAA 399

RESULT 12
AAI92210
ID AAI92210 standard; cDNA; 432 BP.
XX AC AAI92210;
XX AC AAI92210;
XX DT 06-NOV-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 12270.
XX DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation; ss.
XX OS Homo sapiens.
XX OS WO200164835-A2.
XX PN 07-SEP-2001.
XX PD
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XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR P-PSDB; AAO12279.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 1; SEQ ID NO 12270; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 432 BP; 144 A; 86 C; 87 G; 115 T; 0 U; 0 Other;

Query Match 1.1%; Score 22; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GGAAGAAAAAATAATTTTGTG 103
Db 323 GGAAGAAAAAATAATTTTGTG 344

RESULT 13
ABV60815/c
ID ABV60815 standard; cDNA; 468 BP.
XX AC ABV60815;
XX AC ABV60815;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 60806.
XX DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX OS WO200160860-A2.
XX PN 23-AUG-2001.
XX PD 20-FEB-2001; 2001WO-US005171.
XX PF 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX XX
```

PI Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX Claim 1; Page 11567; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 468 BP; 131 A; 114 C; 114 G; 109 T; 0 U; 0 Other;
 Query Match 1.1%; Score 22; DB 5; Length 468;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1590 AAAAAAAAAATTGAAAAAAAAA 1611
 DB 149 AAAAAAAAAATTGAAAAAAAAA 128
 RESULT 14
 ID ADS51475/c
 XX ADS51475 standard; cDNA; 2115 BP.
 AC ADS51475;
 XX
 XX 02-DEC-2004 (first entry)
 DT Bacterial polynucleotide #6218.
 DE Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX Bacteria.
 OS US2003233675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR (CAOY/) CAO Y.
 XX (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX Claim 1; SEQ ID NO 29905; 122pp; English.
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 2115 BP; 738 A; 339 C; 336 G; 702 T; 0 U; 0 Other;
 Query Match 1.1%; Score 22; DB 13; Length 2115;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1589 CAAAAAAAAATTGAAAAAAAAA 1610
 DB 53 CAAAAAAAAATTGAAAAAAAAA 32
 RESULT 15
 AAV52213/c
 ID AAV52213 standard; DNA; 9607 BP.
 XX AAV52213;
 AC AAV52213;
 XX 23-OCT-1998 (first entry)
 DT Streptococcus pneumoniae genome fragment SEQ ID NO:80.
 DE Streptococcus pneumoniae
 XX Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
 KW computer readable medium; vaccine; pharmaceutical composition; ds.
 KW Streptococcus pneumoniae.
 OS WO9818931-A2.
 PN
 XX 07-MAY-1998.
 PD
 XX 30-OCT-1997; 97WO-US019588.
 PF
 XX 31-OCT-1996; 96US-0029960P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Kunsch CA, Choi GH, Dillon PJ, Rosen CA, Baraash SC, Fannon M;
 PI Dougherty BA;
 XX WPI; 1998-272225/24.
 DR Computer-readable medium with recorded Streptococcus pneumoniae
 PT polynucleotide sequences - useful in diagnostic kits and assays, and

PT pharmaceutical compositions and vaccines for Streptococcus pneumoniae.
XX
PS Claim 1; Page 637-642; 1409pp; English.
XX
CC The present invention describes a computer readable medium which has the
CC nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded
CC on it, or a representative fragment or a sequence at least 95% identical
CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1
CC to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus
CC pneumoniae. The present invention also describes an isolated nucleic acid
CC molecule encoding a homologue of any of the fragments of the S.pneumoniae
CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
CC by a process comprising: (a) screening a genomic DNA library using as a
CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 to
CC 391, identifying members of the library which contain sequences that
CC hybridize to the target sequence and isolating the nucleic acid molecules
CC from the members; or (b) isolating mRNA, DNA or cDNA produced from an
CC organism, amplifying nucleic acid molecules whose nucleotide sequence is
CC homologous to amplification primers derived from the fragment of the S.
CC pneumoniae genome to prime the amplification and isolating the amplified
CC sequences. The computer readable medium can be used in a computer-based
CC system for identifying fragments of the S. pneumoniae genome of
CC commercial importance, or expression modulating fragments of the S.
CC pneumoniae genome. Products from the present invention can be used in
CC diagnosis kits and assays, and pharmaceutical compositions and vaccines
CC for S. pneumoniae
XX
SQ Sequence 9607 BP; 2789 A; 1852 C; 2311 G; 2655 T; 0 U; 0 Other;

Query Match 1.1%; Score 22; DB 2; Length 9607;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 TTCTCTTTCTATTATT 53
Db 8125 TTCTCTTTCTATTATT 8104

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Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

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- 5: /cgn2_6/prodata/1/ina/6C COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	22	1.1	9607	3	US-08-961-527-80
C 2	21	1.0	2267	3	US-09-142-569-5
C 3	21	1.0	2267	4	US-09-495-448A-5
C 4	21	1.0	2338	4	US-09-582-337-1
C 5	21	1.0	2350	3	US-09-187-478-1
C 6	21	1.0	2350	3	US-09-292-036-1
C 7	21	1.0	40742	4	US-09-949-016-11751
C 8	21	1.0	40747	4	US-09-949-016-13097
C 9	20	1.0	20	4	US-09-823-634A-13
C 10	20	1.0	20	4	US-09-823-647B-13
C 11	20	1.0	240	4	US-09-248-796A-8498
C 12	20	1.0	381	4	US-09-601-198-173
C 13	20	1.0	425	4	US-09-786-454A-1
C 14	20	1.0	601	4	US-09-949-016-28079
C 15	20	1.0	601	4	US-09-949-016-42035
C 16	20	1.0	601	4	US-09-949-016-42036
C 17	20	1.0	601	4	US-09-949-016-162196
C 18	20	1.0	1094	3	US-09-173-914-5
C 19	20	1.0	52874	4	US-09-949-016-14868
C 20	20	1.0	56131	4	US-09-949-016-12944
C 21	20	1.0	64291	4	US-09-949-016-16278
C 22	20	1.0	86947	4	US-09-949-016-11930
C 23	20	1.0	117410	4	US-09-949-016-12282
C 24	20	1.0	149971	4	US-09-949-016-13590
C 25	20	1.0	450395	4	US-09-949-016-15473
C 26	19	0.9	140	4	US-09-513-999C-33553
C 27	19	0.9	303	4	US-09-248-796A-10927
C 28	19	0.9	19	19	Sequence 80, Appl
C 29	19	0.9	19	19	Sequence 5, Appl
C 30	19	0.9	19	19	Sequence 5, Appl
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Sequence 2580, Ap
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Sequence 41952, A
Sequence 70744, A
Sequence 70745, A
Sequence 70746, A
Sequence 135273, A
Sequence 137471, A
Sequence 137472, A
Sequence 137473, A
Sequence 137474, A
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Sequence 137476, A
Sequence 186625, A
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Sequence 6, Appl
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Sequence 13, Appl
Sequence 14643, A
Sequence 3438, Ap
Sequence 1858, Ap
Sequence 125, App
Sequence 7, Appl
Sequence 45, Appl
Sequence 7, Appl
Sequence 45, Appl
Sequence 49, Appl
Sequence 94, Appl
Sequence 11947, A
Sequence 21, Appl
Sequence 87, Appl
Sequence 12585, A
Sequence 17306, A
Sequence 14268, A
Sequence 1748, A
Sequence 13591, A
Sequence 14759, A
Sequence 17589, A
Sequence 13499, A
Sequence 13779, A
Sequence 13608, A
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Sequence 12890, A
Sequence 16344, A
Sequence 13768, A
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Sequence 13634, A
Sequence 15532, A
Sequence 16597, A
Sequence 17074, A
Sequence 15127, A
Sequence 12930, A
Sequence 12938, A

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c 102	19	0.9	187580	4	US-09-949-016-13266	Sequence 13266, A	175	18	0.9	601	4	US-09-949-016-173723	Sequence 173723, A
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c 104	19	0.9	246240	2	US-08-724-394A-20	Sequence 20, Appl	177	18	0.9	601	4	US-09-949-016-180103	Sequence 180103, A
c 105	19	0.9	246240	2	US-08-724-394A-21	Sequence 21, Appl	178	18	0.9	601	4	US-09-949-016-180104	Sequence 180104, A
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c 107	19	0.9	256171	4	US-09-949-016-12822	Sequence 12822, A	c 180	18	0.9	601	4	US-09-949-016-186115	Sequence 186115, A
c 108	19	0.9	256176	4	US-09-949-016-15524	Sequence 15524, A	181	18	0.9	606	3	US-09-385-982-60	Sequence 60, Appl
c 109	19	0.9	275110	4	US-09-949-016-12706	Sequence 12706, A	182	18	0.9	650	3	US-08-943-731-61	Sequence 61, Appl
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c 113	19	0.9	784019	4	US-09-949-016-14033	Sequence 14033, A	c 186	18	0.9	972	4	US-09-107-532A-1075	Sequence 1075, Ap
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c 115	19	0.9	828152	4	US-09-949-016-12777	Sequence 12777, A	c 188	18	0.9	1027	4	US-09-270-767-5517	Sequence 5517, Ap
c 116	18	0.9	180	4	US-09-270-767-26807	Sequence 26807, A	c 189	18	0.9	1027	4	US-09-270-767-20799	Sequence 20799, A
c 117	18	0.9	186	4	US-09-248-796A-8139	Sequence 8139, Ap	c 190	18	0.9	1039	4	US-09-270-767-1746	Sequence 1746, Ap
c 118	18	0.9	217	4	US-09-513-999C-26675	Sequence 26675, A	c 191	18	0.9	1039	4	US-09-270-767-17028	Sequence 17028, A
c 119	18	0.9	237	4	US-09-248-796A-9549	Sequence 9549, Ap	c 192	18	0.9	1074	4	US-09-396-149-19	Sequence 19, Appl
c 120	18	0.9	238	4	US-09-313-294A-2395	Sequence 2395, Ap	c 193	18	0.9	1123	4	US-09-270-767-12906	Sequence 12906, A
c 121	18	0.9	246	3	US-09-134-001C-1103	Sequence 1103, Ap	c 194	18	0.9	1146	4	US-09-248-796A-138	Sequence 138, App
c 122	18	0.9	252	4	US-09-248-796A-8879	Sequence 8879, Ap	c 195	18	0.9	1318	4	US-09-843-472-7	Sequence 7, Appl1
c 123	18	0.9	336	3	US-09-134-001C-691	Sequence 691, App	c 196	18	0.9	1446	4	US-09-270-767-26149	Sequence 26149, A
c 124	18	0.9	339	3	US-09-134-001C-140	Sequence 140, App	c 197	18	0.9	1485	4	US-09-134-000C-2345	Sequence 2345, Ap
c 125	18	0.9	351	4	US-09-248-796A-12909	Sequence 12909, A	c 198	18	0.9	1496	2	US-08-031-538-5	Sequence 5, Appl1
c 126	18	0.9	359	3	US-09-423-233-23	Sequence 23, Appl	c 199	18	0.9	1605	4	US-09-363-247-18	Sequence 18, Appl
c 127	18	0.9	369	4	US-09-513-999C-25019	Sequence 25019, A	c 200	18	0.9	1761	3	US-09-404-879A-387	Sequence 387, App
c 128	18	0.9	438	4	US-09-248-796A-7056	Sequence 7056, Ap	c 201	18	0.9	1761	4	US-09-667-857-387	Sequence 387, App
c 129	18	0.9	498	4	US-09-107-532A-3376	Sequence 3376, Ap	c 202	18	0.9	1767	4	US-09-601-198-72	Sequence 72, Appl
c 130	18	0.9	530	4	US-09-270-767-7029	Sequence 7029, Ap	c 203	18	0.9	1827	4	US-09-248-796A-301	Sequence 301, App
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c 136	18	0.9	601	4	US-09-949-016-30010	Sequence 30010, A	c 209	18	0.9	2136	4	US-09-134-000C-2065	Sequence 2065, Ap
c 137	18	0.9	601	4	US-09-949-016-37283	Sequence 37283, A	c 210	18	0.9	2445	4	US-09-248-796A-6685	Sequence 6685, Ap
c 138	18	0.9	601	4	US-09-949-016-41718	Sequence 41718, A	c 211	18	0.9	2608	3	US-09-404-879A-386	Sequence 386, App
c 139	18	0.9	601	4	US-09-949-016-41719	Sequence 41719, A	c 212	18	0.9	2608	4	US-09-667-857-386	Sequence 386, App
c 140	18	0.9	601	4	US-09-949-016-41720	Sequence 41720, A	c 213	18	0.9	2901	4	US-09-710-279-3410	Sequence 3410, Ap
c 141	18	0.9	601	4	US-09-949-016-42565	Sequence 42565, A	c 214	18	0.9	2943	3	US-09-404-879A-385	Sequence 385, App
c 142	18	0.9	601	4	US-09-949-016-45542	Sequence 45542, A	c 215	18	0.9	2943	4	US-09-667-857-385	Sequence 385, App
c 143	18	0.9	601	4	US-09-949-016-47839	Sequence 47839, A	c 216	18	0.9	2996	3	US-09-404-879A-311	Sequence 311, App
c 144	18	0.9	601	4	US-09-949-016-52554	Sequence 52554, A	c 217	18	0.9	2996	4	US-09-338-933-311	Sequence 311, App
c 145	18	0.9	601	4	US-09-949-016-54997	Sequence 54997, A	c 218	18	0.9	2996	4	US-09-667-857-311	Sequence 311, App
c 146	18	0.9	601	4	US-09-949-016-63260	Sequence 63260, A	c 219	18	0.9	3015	4	US-09-710-279-3401	Sequence 3401, Ap
c 147	18	0.9	601	4	US-09-949-016-63261	Sequence 63261, A	c 220	18	0.9	3110	3	US-08-936-165A-257	Sequence 257, App
c 148	18	0.9	601	4	US-09-949-016-82593	Sequence 82593, A	c 221	18	0.9	3222	4	US-08-714-741-39	Sequence 39, Appl
c 149	18	0.9	601	4	US-09-949-016-88051	Sequence 88051, A	c 222	18	0.9	3291	1	US-08-021-601-1	Sequence 1, Appl1
c 150	18	0.9	601	4	US-09-949-016-88052	Sequence 88052, A	c 223	18	0.9	3291	1	US-08-082-8498-1	Sequence 1, Appl1
c 151	18	0.9	601	4	US-09-949-016-88053	Sequence 88053, A	c 224	18	0.9	3291	5	PCT-US94-01624-1	Sequence 1, Appl1
c 152	18	0.9	601	4	US-09-949-016-88054	Sequence 88054, A	c 225	18	0.9	3807	4	US-09-949-016-5238	Sequence 5238, Ap
c 153	18	0.9	601	4	US-09-949-016-88055	Sequence 88055, A	c 226	18	0.9	3835	4	US-09-710-279-3433	Sequence 3433, Ap
c 154	18	0.9	601	4	US-09-949-016-89154	Sequence 89154, A	c 227	18	0.9	3993	4	US-09-710-279-3985	Sequence 3985, Ap
c 155	18	0.9	601	4	US-09-949-016-89155	Sequence 89155, A	c 228	18	0.9	6676	4	US-09-949-016-16533	Sequence 16533, A
c 156	18	0.9	601	4	US-09-949-016-105699	Sequence 105699, A	c 229	18	0.9	8107	4	US-09-335-586-3	Sequence 3, Appl1
c 157	18	0.9	601	4	US-09-949-016-105700	Sequence 105700, A	c 230	18	0.9	8612	4	US-09-949-016-16810	Sequence 16810, A
c 158	18	0.9	601	4	US-09-949-016-126378	Sequence 126378, A	c 231	18	0.9	10007	3	US-09-410-464-13	Sequence 13, Appl
c 159	18	0.9	601	4	US-09-949-016-126379	Sequence 126379, A	c 232	18	0.9	10470	4	US-08-956-171E-20	Sequence 20, Appl
c 160	18	0.9	601	4	US-09-949-016-128453	Sequence 128453, A	c 233	18	0.9	10470	4	US-08-781-986A-20	Sequence 20, Appl
c 161	18	0.9	601	4	US-09-949-016-131765	Sequence 131765, A	c 234	18	0.9	12317	4	US-09-949-016-14782	Sequence 14782, A
c 162	18	0.9	601	4	US-09-949-016-132236	Sequence 132236, A	c 235	18	0.9	12366	4	US-09-949-016-13082	Sequence 13082, A
c 163	18	0.9	601	4	US-09-949-016-132237	Sequence 132237, A	c 236	18	0.9	12860	4	US-09-949-016-12223	Sequence 12223, A
c 164	18	0.9	601	4	US-09-949-016-148692	Sequence 148692, A	c 237	18	0.9	12861	4	US-09-949-016-13426	Sequence 13426, A
c 165	18	0.9	601	4	US-09-949-016-150377	Sequence 150377, A	c 238	18	0.9	14273	3	US-08-961-527-40	Sequence 40, Appl
c 166	18	0.9	601	4	US-09-949-016-152609	Sequence 152609, A	c 239	18	0.9	16883	4	US-09-949-016-14694	Sequence 14694, A
c 167	18	0.9	601	4	US-09-949-016-152610	Sequence 152610, A	c 240	18	0.9	18591	4	US-09-949-016-14719	Sequence 14719, A
c 168	18	0.9	601	4	US-09-949-016-152611	Sequence 152611, A	c 241	18	0.9	20599	4	US-09-949-016-14477	Sequence 14477, A
c 169	18	0.9	601	4	US-09-949-016-152612	Sequence 152612, A	c 242	18	0.9	20599	4	US-09-949-016-14478	Sequence 14478, A
c 170	18	0.9	601	4	US-09-949-016-152613	Sequence 152613, A	c 243	18	0.9	23766	4	US-09-949-016-13569	Sequence 13569, A
c 171	18	0.9	601	4	US-09-949-016-152862	Sequence 152862, A	c 244	18	0.9	23781	4	US-09-949-016-13446	Sequence 13446, A
c 172	18	0.9	601	4	US-09-949-016-158992	Sequence 158992, A	c 245	18	0.9	24639	4	US-09-949-016-14068	Sequence 14068, A
c 173	18	0.9	601	4	US-09-949-016-160739	Sequence 160739, A	c 246	18	0.9	24715	4	US-09-949-016-12979	Sequence 12979, A

c 247	18	0.9	27491	4	US-09-949-016-12442	Sequence 12442, A	320	18	0.9	121068	4	US-09-949-016-14138	Sequence 14138, A
c 248	18	0.9	28283	4	US-09-949-016-12548	Sequence 12548, A	c 321	18	0.9	123513	4	US-09-949-016-15794	Sequence 15794, A
c 249	18	0.9	28393	4	US-09-949-016-16980	Sequence 16980, A	c 322	18	0.9	124480	4	US-09-949-016-15921	Sequence 15921, A
c 250	18	0.9	29671	4	US-09-949-016-12229	Sequence 12229, A	c 323	18	0.9	128175	4	US-09-949-016-16268	Sequence 16268, A
c 251	18	0.9	29671	4	US-09-949-016-17105	Sequence 17105, A	c 324	18	0.9	129899	4	US-09-949-016-16884	Sequence 16884, A
c 252	18	0.9	29717	4	US-09-949-016-16284	Sequence 16284, A	c 325	18	0.9	135667	4	US-09-949-016-15051	Sequence 15051, A
c 253	18	0.9	29769	4	US-09-949-016-16422	Sequence 16422, A	c 326	18	0.9	141158	4	US-09-949-016-11755	Sequence 11755, A
c 254	18	0.9	30324	4	US-09-949-016-16037	Sequence 16037, A	c 327	18	0.9	144158	4	US-09-949-016-12936	Sequence 12936, A
c 255	18	0.9	31000	4	US-09-966-451-10	Sequence 10, Appl	c 328	18	0.9	147321	4	US-09-949-016-15450	Sequence 15450, A
c 256	18	0.9	33109	4	US-09-949-016-14301	Sequence 14301, A	c 329	18	0.9	148156	4	US-09-949-016-11776	Sequence 11776, A
c 257	18	0.9	33870	4	US-09-949-016-16306	Sequence 16306, A	c 330	18	0.9	149371	4	US-09-949-016-13590	Sequence 13590, A
c 258	18	0.9	34855	4	US-09-949-016-13004	Sequence 13004, A	c 331	18	0.9	150597	4	US-09-949-016-13579	Sequence 13579, A
c 259	18	0.9	35282	4	US-09-949-016-13265	Sequence 13265, A	c 332	18	0.9	152231	3	US-09-128-155-16	Sequence 16, Appl
c 260	18	0.9	38326	4	US-09-949-016-15943	Sequence 15943, A	c 333	18	0.9	152486	4	US-09-949-016-12869	Sequence 12869, A
c 261	18	0.9	38682	3	US-08-943-731-2	Sequence 2, Appl	c 334	18	0.9	155019	4	US-09-949-016-16029	Sequence 16029, A
c 262	18	0.9	39755	4	US-09-949-016-17352	Sequence 17352, A	c 335	18	0.9	155517	4	US-09-949-016-16191	Sequence 16191, A
c 263	18	0.9	40219	4	US-09-949-016-15337	Sequence 15337, A	c 336	18	0.9	155517	4	US-09-949-016-16191	Sequence 16191, A
c 264	18	0.9	40315	4	US-09-949-016-11753	Sequence 11753, A	c 337	18	0.9	161124	4	US-09-949-016-11760	Sequence 11760, A
c 265	18	0.9	40649	4	US-09-949-016-14219	Sequence 14219, A	c 338	18	0.9	178884	4	US-09-949-016-12733	Sequence 12733, A
c 266	18	0.9	41100	4	US-09-755-665-46	Sequence 46, Appl	c 339	18	0.9	178884	4	US-09-949-016-13039	Sequence 13039, A
c 267	18	0.9	41639	4	US-09-949-016-15471	Sequence 15471, A	c 340	18	0.9	181251	4	US-09-949-016-15970	Sequence 15970, A
c 268	18	0.9	43576	4	US-09-676-519-19	Sequence 19, Appl	c 341	18	0.9	183770	4	US-09-949-016-15546	Sequence 15546, A
c 269	18	0.9	44244	4	US-09-949-016-11743	Sequence 11743, A	c 342	18	0.9	187595	4	US-09-949-016-15546	Sequence 15546, A
c 270	18	0.9	44244	4	US-09-949-016-13579	Sequence 13579, A	c 343	18	0.9	203475	4	US-09-949-016-14517	Sequence 14517, A
c 271	18	0.9	44342	4	US-09-949-016-12661	Sequence 12661, A	c 344	18	0.9	203475	4	US-09-949-016-14518	Sequence 14518, A
c 272	18	0.9	44821	4	US-09-949-016-13764	Sequence 13764, A	c 345	18	0.9	203475	4	US-09-949-016-14519	Sequence 14519, A
c 273	18	0.9	45183	4	US-09-949-016-12798	Sequence 12798, A	c 346	18	0.9	203475	4	US-09-949-016-17226	Sequence 17226, A
c 274	18	0.9	47419	4	US-09-949-016-11841	Sequence 11841, A	c 347	18	0.9	203475	4	US-09-949-016-17227	Sequence 17227, A
c 275	18	0.9	47420	4	US-09-949-016-15484	Sequence 15484, A	c 348	18	0.9	203475	4	US-09-949-016-17228	Sequence 17228, A
c 276	18	0.9	56302	4	US-09-949-016-11892	Sequence 11892, A	c 349	18	0.9	222452	4	US-09-949-016-12968	Sequence 12968, A
c 277	18	0.9	57392	4	US-09-949-016-12070	Sequence 12070, A	c 350	18	0.9	222452	4	US-09-949-016-11842	Sequence 11842, A
c 278	18	0.9	57402	4	US-09-949-016-13293	Sequence 13293, A	c 351	18	0.9	227979	4	US-09-949-016-17127	Sequence 17127, A
c 279	18	0.9	57875	4	US-09-949-016-13152	Sequence 13152, A	c 352	18	0.9	228896	4	US-09-949-016-17127	Sequence 17127, A
c 280	18	0.9	60376	4	US-09-949-016-12423	Sequence 12423, A	c 353	18	0.9	237510	4	US-09-949-016-14273	Sequence 14273, A
c 281	18	0.9	63563	4	US-09-596-002-33	Sequence 33, Appl	c 354	18	0.9	312474	4	US-09-949-016-17434	Sequence 17434, A
c 282	18	0.9	64467	4	US-09-803-6718-3	Sequence 3, Appl	c 355	18	0.9	319608	4	US-09-539-333D-1	Sequence 1, Appl
c 283	18	0.9	64667	4	US-10-274-409-3	Sequence 3, Appl	c 356	18	0.9	319608	4	US-09-679-409-1	Sequence 1, Appl
c 284	18	0.9	68444	4	US-09-949-016-13968	Sequence 13968, A	c 357	18	0.9	390416	4	US-09-949-016-16923	Sequence 16923, A
c 285	18	0.9	69874	4	US-09-949-016-12361	Sequence 12361, A	c 358	18	0.9	636591	4	US-09-949-016-11808	Sequence 11808, A
c 286	18	0.9	69874	4	US-09-949-016-13049	Sequence 13049, A	c 359	18	0.9	636591	4	US-09-949-016-13388	Sequence 13388, A
c 287	18	0.9	72992	4	US-09-949-016-17592	Sequence 17592, A	c 360	18	0.9	640681	4	US-09-790-988-1	Sequence 1, Appl
c 288	18	0.9	72992	4	US-09-949-016-17592	Sequence 17592, A	c 361	18	0.9	670689	4	US-09-949-016-12505	Sequence 12505, A
c 289	18	0.9	76281	4	US-09-949-016-12708	Sequence 12708, A	c 362	18	0.9	670690	4	US-09-949-016-14207	Sequence 14207, A
c 290	18	0.9	80355	4	US-09-949-016-12735	Sequence 12735, A	c 363	18	0.9	767677	4	US-09-949-016-12147	Sequence 12147, A
c 291	18	0.9	80357	4	US-09-949-016-12352	Sequence 12352, A	c 364	18	0.9	767677	4	US-09-949-016-17361	Sequence 17361, A
c 292	18	0.9	81819	4	US-09-949-016-16661	Sequence 16661, A	c 365	18	0.9	1230025	4	US-09-198-452A-1	Sequence 1, Appl
c 293	18	0.9	81819	4	US-09-949-016-16661	Sequence 16661, A	c 366	18	0.9	1230025	4	US-09-438-185A-1	Sequence 1, Appl
c 294	18	0.9	84132	4	US-09-949-016-16241	Sequence 16241, A	c 367	18	0.9	1664976	4	US-08-916-421B-1	Sequence 1, Appl
c 295	18	0.9	85122	4	US-09-949-016-14693	Sequence 14693, A	c 368	18	0.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
c 296	18	0.9	85963	4	US-09-949-016-13804	Sequence 13804, A	c 369	17	0.8	17	4	US-09-866-108A-9901	Sequence 9901, Ap
c 297	18	0.9	87350	3	US-08-781-891-79	Sequence 79, Appl	c 370	17	0.8	25	4	US-09-866-108A-14793	Sequence 14793, A
c 298	18	0.9	87350	4	US-09-618-166-79	Sequence 79, Appl	c 371	17	0.8	25	4	US-09-866-108A-14794	Sequence 14794, A
c 299	18	0.9	87543	3	US-09-791-211-3	Sequence 3, Appl	c 372	17	0.8	25	4	US-09-866-108A-14795	Sequence 14795, A
c 300	18	0.9	87567	4	US-09-949-016-13335	Sequence 13335, A	c 373	17	0.8	25	4	US-09-866-108A-14796	Sequence 14796, A
c 301	18	0.9	88240	4	US-09-949-016-16279	Sequence 16279, A	c 374	17	0.8	25	4	US-09-866-108A-14797	Sequence 14797, A
c 302	18	0.9	90150	4	US-09-949-016-17383	Sequence 17383, A	c 375	17	0.8	25	4	US-09-866-108A-14798	Sequence 14798, A
c 303	18	0.9	92227	4	US-09-949-016-11929	Sequence 11929, A	c 376	17	0.8	25	4	US-09-866-108A-14799	Sequence 14799, A
c 304	18	0.9	92232	4	US-09-949-016-15421	Sequence 15421, A	c 377	17	0.8	25	4	US-09-866-108A-14800	Sequence 14800, A
c 305	18	0.9	93920	4	US-09-949-016-12461	Sequence 12461, A	c 378	17	0.8	25	4	US-09-866-108A-14801	Sequence 14801, A
c 306	18	0.9	93920	4	US-09-949-016-16853	Sequence 16853, A	c 379	17	0.8	25	4	US-09-396-1966-78732	Sequence 78732, A
c 307	18	0.9	95648	4	US-09-949-016-13139	Sequence 13139, A	c 380	17	0.8	57	4	US-08-956-171B-1697	Sequence 1697, Ap
c 308	18	0.9	96922	4	US-09-949-016-17061	Sequence 17061, A	c 381	17	0.8	67	4	US-08-781-986A-1697	Sequence 1697, Ap
c 309	18	0.9	100836	4	US-09-949-016-12871	Sequence 12871, A	c 382	17	0.8	86	4	US-09-513-999C-16587	Sequence 16587, A
c 310	18	0.9	100837	4	US-09-949-016-17063	Sequence 17063, A	c 383	17	0.8	86	4	US-09-792-024-141	Sequence 141, App
c 311	18	0.9	100877	4	US-09-949-016-13276	Sequence 13276, A	c 384	17	0.8	102	4	US-09-513-999C-21511	Sequence 21511, A
c 312	18	0.9	100928	4	US-09-949-016-16926	Sequence 16926, A	c 385	17	0.8	110	4	US-09-513-999C-13479	Sequence 13479, A
c 313	18	0.9	101128	4	US-09-949-016-14293	Sequence 14293, A	c 386	17	0.8	132	4	US-08-956-171B-1263	Sequence 1263, Ap
c 314	18	0.9	103987	4	US-09-949-016-12513	Sequence 12513, A	c 387	17	0.8	132	4	US-08-781-986A-1263	Sequence 1263, Ap
c 315	18	0.9	103988	4	US-09-949-016-12513	Sequence 12513, A	c 388	17	0.8	134	4	US-09-270-767-31580	Sequence 31580, A
c 316	18	0.9	106199	4	US-09-949-016-12393	Sequence 12393, A	c 389	17	0.8	142	4	US-09-513-999C-24222	Sequence 24222, A
c 317	18	0.9	107980	4	US-09-949-016-14370	Sequence 14370, A	c 390	17	0.8	146	4	US-09-621-976-14975	Sequence 14975, A
c 318	18	0.9	112112	4	US-09-949-016-15639	Sequence 15639, A	c 391	17	0.8	168	1	US-08-691-641-16	Sequence 16, Appl
c 319	18	0.9	119214	4	US-09-949-016-12507	Sequence 12507, A	c 392	17	0.8	171	4	US-09-513-999C-17881	Sequence 17881, A

C 393	17	0.8	183	4	US-09-248-796A-10444	Sequence 10444, A	C 465	17	0.8	368	4	US-09-270-767-6135	Sequence 6135, Ap
C 394	17	0.8	199	1	US-08-330-108-4	Sequence 4, Appl1	C 467	17	0.8	368	4	US-09-270-767-21417	Sequence 21417, A
C 395	17	0.8	199	5	PCT-US92-10087-4	Sequence 4, Appl1	C 469	17	0.8	369	4	US-09-248-796A-9541	Sequence 9541, Ap
C 396	17	0.8	204	4	US-09-248-796A-10679	Sequence 10679, A	C 469	17	0.8	371	4	US-09-621-976-16048	Sequence 16048, A
C 397	17	0.8	205	4	US-08-956-171E-2401	Sequence 2401, Ap	C 470	17	0.8	387	4	US-09-270-767-2955	Sequence 2955, Ap
C 398	17	0.8	205	4	US-08-781-986A-2401	Sequence 2401, Ap	C 471	17	0.8	387	4	US-09-270-767-18237	Sequence 18237, A
C 399	17	0.8	206	4	US-09-513-999C-19662	Sequence 19662, A	C 472	17	0.8	391	4	US-09-703-705-57	Sequence 57, Appl
C 400	17	0.8	207	4	US-09-248-796A-8940	Sequence 8940, Ap	C 473	17	0.8	391	4	US-09-736-457-57	Sequence 57, Appl
C 401	17	0.8	207	4	US-09-248-796A-11501	Sequence 11501, A	C 474	17	0.8	391	4	US-09-614-124B-57	Sequence 57, Appl
C 402	17	0.8	210	4	US-09-543-681A-326	Sequence 326, App	C 475	17	0.8	391	4	US-09-671-325-57	Sequence 57, Appl
C 403	17	0.8	216	4	US-09-270-767-8716	Sequence 8716, Ap	C 476	17	0.8	391	4	US-09-589-184-57	Sequence 57, Appl
C 404	17	0.8	216	4	US-09-543-681A-2091	Sequence 2091, Ap	C 477	17	0.8	391	4	US-09-658-824-57	Sequence 57, Appl
C 405	17	0.8	218	4	US-09-513-999C-17093	Sequence 2398A, A	C 477	17	0.8	399	4	US-09-270-767-2976	Sequence 2976, Ap
C 406	17	0.8	261	4	US-09-248-796A-11472	Sequence 11472, A	C 478	17	0.8	399	4	US-09-270-767-18258	Sequence 18258, A
C 407	17	0.8	270	4	US-09-248-796A-7983	Sequence 7983, Ap	C 479	17	0.8	402	3	US-09-134-001C-1967	Sequence 1967, Ap
C 408	17	0.8	272	4	US-09-621-976-16007	Sequence 16007, A	C 480	17	0.8	408	4	US-09-248-796A-8101	Sequence 8101, Ap
C 409	17	0.8	276	4	US-09-543-681A-2091	Sequence 16034, A	C 481	17	0.8	441	4	US-09-621-976-9912	Sequence 9912, Ap
C 410	17	0.8	276	4	US-09-621-976-16039	Sequence 2091, Ap	C 482	17	0.8	441	4	US-09-248-796A-3289	Sequence 3289, Ap
C 411	17	0.8	278	4	US-09-313-294A-1578	Sequence 16039, A	C 483	17	0.8	441	4	US-09-270-767-15243	Sequence 15243, A
C 412	17	0.8	279	4	US-09-621-976-16037	Sequence 1578, Ap	C 484	17	0.8	447	4	US-09-270-767-9807	Sequence 9807, Ap
C 413	17	0.8	280	4	US-09-621-976-16046	Sequence 16037, A	C 485	17	0.8	453	4	US-09-270-767-25089	Sequence 25089, A
C 414	17	0.8	281	4	US-09-621-976-16011	Sequence 16046, A	C 486	17	0.8	453	4	US-09-270-767-4088	Sequence 4088, Ap
C 415	17	0.8	281	4	US-09-621-976-16034	Sequence 16011, A	C 487	17	0.8	462	4	US-09-270-767-19370	Sequence 19370, A
C 416	17	0.8	281	4	US-09-621-976-16054	Sequence 16034, A	C 488	17	0.8	462	4	US-09-270-767-9590	Sequence 9590, Ap
C 417	17	0.8	281	4	US-09-621-976-16059	Sequence 16054, A	C 489	17	0.8	468	4	US-09-248-796A-8988	Sequence 8988, Ap
C 418	17	0.8	282	4	US-09-621-976-16016	Sequence 16059, A	C 490	17	0.8	471	4	US-09-270-767-8988	Sequence 8988, Ap
C 419	17	0.8	282	4	US-09-621-976-16029	Sequence 16016, A	C 491	17	0.8	471	4	US-09-270-767-24270	Sequence 24270, A
C 420	17	0.8	282	4	US-09-248-796A-10119	Sequence 16029, A	C 492	17	0.8	472	4	US-09-270-767-6143	Sequence 6143, Ap
C 421	17	0.8	286	4	US-09-621-976-11456	Sequence 10119, A	C 493	17	0.8	472	4	US-09-270-767-21425	Sequence 21425, A
C 422	17	0.8	289	4	US-09-313-294A-6782	Sequence 11456, A	C 494	17	0.8	485	4	US-09-621-976-12239	Sequence 12239, A
C 423	17	0.8	292	4	US-09-621-976-16009	Sequence 6782, Ap	C 495	17	0.8	485	4	US-09-270-767-9590	Sequence 9590, Ap
C 424	17	0.8	296	4	US-09-621-976-16021	Sequence 16009, A	C 496	17	0.8	497	4	US-09-270-767-24872	Sequence 24872, A
C 425	17	0.8	296	4	US-09-621-976-16049	Sequence 16021, A	C 497	17	0.8	500	4	US-09-866-108A-15750	Sequence 15750, A
C 426	17	0.8	297	4	US-09-621-976-16022	Sequence 16049, A	C 498	17	0.8	504	4	US-09-248-796A-1009	Sequence 1009, Ap
C 427	17	0.8	301	4	US-09-270-767-5573	Sequence 16022, A	C 499	17	0.8	525	3	US-08-941-155-1	Sequence 1, Appl1
C 428	17	0.8	301	4	US-09-270-767-20855	Sequence 5573, Ap	C 500	17	0.8	525	3	US-09-872-047-1	Sequence 1, Appl1
C 429	17	0.8	302	4	US-09-621-976-16017	Sequence 20855, A	C 501	17	0.8	543	4	US-09-540-236-1096	Sequence 1096, Ap
C 430	17	0.8	303	4	US-09-328-352-3583	Sequence 16017, A	C 502	17	0.8	543	4	US-09-270-767-8781	Sequence 8781, Ap
C 431	17	0.8	304	4	US-09-621-976-13024	Sequence 3583, Ap	C 503	17	0.8	552	4	US-09-270-767-24063	Sequence 24063, A
C 432	17	0.8	305	4	US-09-621-976-16020	Sequence 13024, A	C 504	17	0.8	567	4	US-09-248-796A-4827	Sequence 4827, Ap
C 433	17	0.8	306	4	US-09-621-976-16014	Sequence 16020, A	C 505	17	0.8	581	3	US-09-020-956-103	Sequence 103, App
C 434	17	0.8	306	4	US-09-621-976-16035	Sequence 16014, A	C 506	17	0.8	581	3	US-09-030-607-103	Sequence 103, App
C 435	17	0.8	306	4	US-09-621-976-16057	Sequence 16035, A	C 507	17	0.8	581	3	US-09-439-313-103	Sequence 103, App
C 436	17	0.8	307	4	US-09-621-976-16030	Sequence 16057, A	C 508	17	0.8	581	3	US-09-352-616A-103	Sequence 103, App
C 437	17	0.8	315	4	US-09-621-976-16028	Sequence 16030, A	C 509	17	0.8	581	3	US-09-232-149A-103	Sequence 103, App
C 438	17	0.8	318	4	US-09-621-976-16040	Sequence 16028, A	C 510	17	0.8	581	4	US-09-159-812-103	Sequence 103, App
C 439	17	0.8	318	4	US-09-248-796A-9989	Sequence 16040, A	C 511	17	0.8	581	4	US-09-636-215-103	Sequence 103, App
C 440	17	0.8	318	4	US-09-513-999C-35723	Sequence 9989, Ap	C 512	17	0.8	581	4	US-09-685-166A-103	Sequence 103, App
C 441	17	0.8	319	4	US-09-621-976-16055	Sequence 35723, A	C 513	17	0.8	581	4	US-09-115-453-103	Sequence 103, App
C 442	17	0.8	320	4	US-09-621-976-16056	Sequence 16055, A	C 514	17	0.8	581	4	US-09-688-489-103	Sequence 103, App
C 443	17	0.8	321	4	US-09-248-796A-13652	Sequence 16056, A	C 515	17	0.8	581	4	US-09-679-426-103	Sequence 103, App
C 444	17	0.8	324	4	US-09-621-976-16027	Sequence 13652, A	C 516	17	0.8	581	4	US-09-759-143-103	Sequence 103, App
C 445	17	0.8	326	4	US-09-621-976-16024	Sequence 16027, A	C 517	17	0.8	581	4	US-09-651-236-103	Sequence 103, App
C 446	17	0.8	326	4	US-09-621-976-16012	Sequence 16024, A	C 518	17	0.8	583	3	US-09-030-607-203	Sequence 203, App
C 447	17	0.8	329	4	US-09-621-976-16052	Sequence 16012, A	C 519	17	0.8	583	3	US-09-439-313-203	Sequence 203, App
C 448	17	0.8	332	4	US-09-621-976-16053	Sequence 16052, A	C 520	17	0.8	583	3	US-09-352-616A-203	Sequence 203, App
C 449	17	0.8	333	4	US-09-621-976-16032	Sequence 16053, A	C 521	17	0.8	583	3	US-09-232-149A-203	Sequence 203, App
C 450	17	0.8	333	4	US-09-621-976-16032	Sequence 16032, A	C 522	17	0.8	583	4	US-09-159-812-203	Sequence 203, App
C 451	17	0.8	334	4	US-09-621-976-16045	Sequence 16045, A	C 523	17	0.8	583	4	US-09-636-215-203	Sequence 203, App
C 452	17	0.8	335	4	US-09-621-976-16038	Sequence 16044, A	C 524	17	0.8	583	4	US-09-685-166A-203	Sequence 203, App
C 453	17	0.8	336	4	US-09-621-976-16013	Sequence 16038, A	C 525	17	0.8	583	4	US-09-115-453-203	Sequence 203, App
C 454	17	0.8	336	4	US-09-248-796A-8946	Sequence 16013, A	C 526	17	0.8	583	4	US-09-688-489-203	Sequence 203, App
C 455	17	0.8	338	4	US-09-621-976-19232	Sequence 8946, Ap	C 527	17	0.8	583	4	US-09-679-426-203	Sequence 203, App
C 456	17	0.8	339	4	US-09-621-976-16015	Sequence 19232, A	C 528	17	0.8	583	4	US-09-759-143-203	Sequence 203, App
C 457	17	0.8	346	4	US-09-513-999C-26181	Sequence 26181, A	C 529	17	0.8	600	4	US-09-651-236-203	Sequence 203, App
C 458	17	0.8	347	4	US-09-621-976-16026	Sequence 16026, A	C 530	17	0.8	600	4	US-09-270-767-6676	Sequence 6676, Ap
C 459	17	0.8	355	4	US-09-621-976-8475	Sequence 8475, Ap	C 531	17	0.8	601	4	US-09-270-767-21958	Sequence 21958, A
C 460	17	0.8	355	4	US-09-621-976-8488	Sequence 8488, Ap	C 532	17	0.8	601	4	US-09-949-016-21343	Sequence 21343, A
C 461	17	0.8	357	4	US-09-621-976-16058	Sequence 16058, A	C 533	17	0.8	601	4	US-09-949-016-22574	Sequence 22574, A
C 462	17	0.8	359	4	US-09-621-976-16008	Sequence 16008, A	C 534	17	0.8	601	4	US-09-949-016-23771	Sequence 23771, A
C 463	17	0.8	359	4	US-09-621-976-16019	Sequence 16019, A	C 535	17	0.8	601	4	US-09-949-016-24951	Sequence 24951, A
C 464	17	0.8	362	4	US-09-621-976-16010	Sequence 16010, A	C 536	17	0.8	601	4	US-09-949-016-25316	Sequence 25316, A
C 465	17	0.8	365	4	US-09-621-976-16042	Sequence 16042, A	C 537	17	0.8	601	4	US-09-949-016-25317	Sequence 25317, A
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541	17	0.8	601	4	US-09-949-016-26153	Sequence 26153, A	C 614	17	0.8	601	4	US-09-949-016-87085	Sequence 87085, A
542	17	0.8	601	4	US-09-949-016-28276	Sequence 28276, A	C 615	17	0.8	601	4	US-09-949-016-87300	Sequence 87300, A
543	17	0.8	601	4	US-09-949-016-28277	Sequence 28277, A	C 616	17	0.8	601	4	US-09-949-016-88382	Sequence 88382, A
544	17	0.8	601	4	US-09-949-016-28287	Sequence 28287, A	C 617	17	0.8	601	4	US-09-949-016-88872	Sequence 88872, A
545	17	0.8	601	4	US-09-949-016-29827	Sequence 29827, A	C 618	17	0.8	601	4	US-09-949-016-88873	Sequence 88873, A
546	17	0.8	601	4	US-09-949-016-31740	Sequence 31740, A	C 619	17	0.8	601	4	US-09-949-016-88874	Sequence 88874, A
547	17	0.8	601	4	US-09-949-016-31741	Sequence 31741, A	C 620	17	0.8	601	4	US-09-949-016-88875	Sequence 88875, A
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551	17	0.8	601	4	US-09-949-016-33332	Sequence 33332, A	C 624	17	0.8	601	4	US-09-949-016-91657	Sequence 91657, A
552	17	0.8	601	4	US-09-949-016-34516	Sequence 34516, A	C 625	17	0.8	601	4	US-09-949-016-91658	Sequence 91658, A
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555	17	0.8	601	4	US-09-949-016-36645	Sequence 36645, A	C 628	17	0.8	601	4	US-09-949-016-93940	Sequence 93940, A
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558	17	0.8	601	4	US-09-949-016-36668	Sequence 36668, A	C 631	17	0.8	601	4	US-09-949-016-105762	Sequence 105762, A
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563	17	0.8	601	4	US-09-949-016-39493	Sequence 39493, A	C 636	17	0.8	601	4	US-09-949-016-108216	Sequence 108216, A
564	17	0.8	601	4	US-09-949-016-39526	Sequence 39526, A	C 637	17	0.8	601	4	US-09-949-016-108217	Sequence 108217, A
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574	17	0.8	601	4	US-09-949-016-52848	Sequence 52848, A	C 647	17	0.8	601	4	US-09-949-016-118509	Sequence 118509, A
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576	17	0.8	601	4	US-09-949-016-55099	Sequence 55099, A	C 649	17	0.8	601	4	US-09-949-016-118575	Sequence 118575, A
577	17	0.8	601	4	US-09-949-016-55099	Sequence 55099, A	C 650	17	0.8	601	4	US-09-949-016-118608	Sequence 118608, A
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581	17	0.8	601	4	US-09-949-016-62050	Sequence 62050, A	C 654	17	0.8	601	4	US-09-949-016-120876	Sequence 120876, A
582	17	0.8	601	4	US-09-949-016-62050	Sequence 62050, A	C 655	17	0.8	601	4	US-09-949-016-121006	Sequence 121006, A
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591	17	0.8	601	4	US-09-949-016-72612	Sequence 72612, A	C 664	17	0.8	601	4	US-09-949-016-124277	Sequence 124277, A
592	17	0.8	601	4	US-09-949-016-73315	Sequence 73315, A	C 665	17	0.8	601	4	US-09-949-016-125473	Sequence 125473, A
593	17	0.8	601	4	US-09-949-016-73315	Sequence 73315, A	C 666	17	0.8	601	4	US-09-949-016-125475	Sequence 125475, A
594	17	0.8	601	4	US-09-949-016-73535	Sequence 73535, A	C 667	17	0.8	601	4	US-09-949-016-126073	Sequence 126073, A
595	17	0.8	601	4	US-09-949-016-74335	Sequence 74335, A	C 668	17	0.8	601	4	US-09-949-016-126385	Sequence 126385, A
596	17	0.8	601	4	US-09-949-016-76583	Sequence 76583, A	C 669	17	0.8	601	4	US-09-949-016-126388	Sequence 126388, A
597	17	0.8	601	4	US-09-949-016-76992	Sequence 76992, A	C 670	17	0.8	601	4	US-09-949-016-126389	Sequence 126389, A
598	17	0.8	601	4	US-09-949-016-77222	Sequence 77222, A	C 671	17	0.8	601	4	US-09-949-016-126420	Sequence 126420, A
599	17	0.8	601	4	US-09-949-016-77781	Sequence 77781, A	C 672	17	0.8	601	4	US-09-949-016-126421	Sequence 126421, A
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602	17	0.8	601	4	US-09-949-016-79155	Sequence 79155, A	C 675	17	0.8	601	4	US-09-949-016-130650	Sequence 130650, A
603	17	0.8	601	4	US-09-949-016-79156	Sequence 79156, A	C 676	17	0.8	601	4	US-09-949-016-130733	Sequence 130733, A
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605	17	0.8	601	4	US-09-949-016-80258	Sequence 80258, A	C 678	17	0.8	601	4	US-09-949-016-130735	Sequence 130735, A
606	17	0.8	601	4	US-09-949-016-80259	Sequence 80259, A	C 679	17	0.8	601	4	US-09-949-016-132707	Sequence 132707, A
607	17	0.8	601	4	US-09-949-016-82260	Sequence 82260, A	C 680	17	0.8	601	4	US-09-949-016-134684	Sequence 134684, A
608	17	0.8	601	4	US-09-949-016-82250	Sequence 82250, A	C 681	17	0.8	601	4	US-09-949-016-134685	Sequence 134685, A
609	17	0.8	601	4	US-09-949-016-82571	Sequence 82571, A	C 682	17	0.8	601	4	US-09-949-016-136377	Sequence 136377, A
610	17	0.8	601	4	US-09-949-016-82572	Sequence 82572, A	C 683	17	0.8	601	4	US-09-949-016-136378	Sequence 136378, A
611	17	0.8	601	4	US-09-949-016-82854	Sequence 82854, A	C 684	17	0.8	601	4	US-09-949-016-137820	Sequence 137820, A

685	17	0.8	601	4	US-09-949-016-139398	Sequence 139398,	c 758	17	0.8	601	4	US-09-949-016-195624	Sequence 185624,
686	17	0.8	601	4	US-09-949-016-139399	Sequence 139399,	c 759	17	0.8	601	4	US-09-949-016-186330	Sequence 186330,
687	17	0.8	601	4	US-09-949-016-139401	Sequence 139401,	c 760	17	0.8	601	4	US-09-949-016-186331	Sequence 186331,
688	17	0.8	601	4	US-09-949-016-139402	Sequence 139402,	c 761	17	0.8	601	4	US-09-949-016-186332	Sequence 186332,
c 689	17	0.8	601	4	US-09-949-016-140114	Sequence 140114,	c 762	17	0.8	601	4	US-09-949-016-186367	Sequence 186367,
c 690	17	0.8	601	4	US-09-949-016-140156	Sequence 140156,	c 763	17	0.8	601	4	US-09-949-016-188211	Sequence 188211,
c 691	17	0.8	601	4	US-09-949-016-140157	Sequence 140157,	c 764	17	0.8	601	4	US-09-949-016-189366	Sequence 189366,
c 692	17	0.8	601	4	US-09-949-016-141922	Sequence 141922,	c 765	17	0.8	601	4	US-09-949-016-189368	Sequence 189368,
c 693	17	0.8	601	4	US-09-949-016-141923	Sequence 141923,	c 766	17	0.8	601	4	US-09-949-016-191234	Sequence 191234,
c 694	17	0.8	601	4	US-09-949-016-143177	Sequence 143177,	c 767	17	0.8	601	4	US-09-949-016-193978	Sequence 193978,
c 695	17	0.8	601	4	US-09-949-016-143178	Sequence 143178,	c 768	17	0.8	601	4	US-09-949-016-194598	Sequence 194598,
c 696	17	0.8	601	4	US-09-949-016-143738	Sequence 143738,	c 769	17	0.8	601	4	US-09-949-016-194599	Sequence 194599,
c 697	17	0.8	601	4	US-09-949-016-144367	Sequence 144367,	c 770	17	0.8	601	4	US-09-949-016-194903	Sequence 194903,
c 698	17	0.8	601	4	US-09-949-016-144968	Sequence 144968,	c 771	17	0.8	601	4	US-09-949-016-194976	Sequence 194976,
c 699	17	0.8	601	4	US-09-949-016-149453	Sequence 149453,	c 772	17	0.8	601	4	US-09-949-016-194977	Sequence 194977,
c 700	17	0.8	601	4	US-09-949-016-149454	Sequence 149454,	c 773	17	0.8	601	4	US-09-949-016-196879	Sequence 196879,
701	17	0.8	601	4	US-09-949-016-151634	Sequence 151634,	c 774	17	0.8	601	4	US-09-949-016-196880	Sequence 196880,
c 702	17	0.8	601	4	US-09-949-016-152576	Sequence 152576,	c 775	17	0.8	601	4	US-09-949-016-197896	Sequence 197896,
c 703	17	0.8	601	4	US-09-949-016-153001	Sequence 153001,	c 776	17	0.8	601	4	US-09-949-016-198544	Sequence 198544,
c 704	17	0.8	601	4	US-09-949-016-153399	Sequence 153399,	c 777	17	0.8	601	4	US-09-949-016-198545	Sequence 198545,
c 705	17	0.8	601	4	US-09-949-016-153401	Sequence 153401,	c 778	17	0.8	601	4	US-09-949-016-199144	Sequence 199144,
c 706	17	0.8	601	4	US-09-949-016-153402	Sequence 153402,	c 779	17	0.8	601	4	US-09-949-016-206692	Sequence 206692,
c 707	17	0.8	601	4	US-09-949-016-153824	Sequence 153824,	c 780	17	0.8	602	4	US-09-799-451-72	Sequence 72, Appl
708	17	0.8	601	4	US-09-949-016-154976	Sequence 154976,	c 781	17	0.8	614	4	US-09-902-540-1318	Sequence 1318, Ap
c 709	17	0.8	601	4	US-09-949-016-155006	Sequence 155006,	c 782	17	0.8	618	4	US-09-270-767-7128	Sequence 7128, Ap
c 710	17	0.8	601	4	US-09-949-016-156270	Sequence 156270,	c 783	17	0.8	618	4	US-09-270-767-22410	Sequence 22410, A
c 711	17	0.8	601	4	US-09-949-016-157408	Sequence 157408,	c 784	17	0.8	635	4	US-09-270-767-3442	Sequence 3442, Ap
c 712	17	0.8	601	4	US-09-949-016-157409	Sequence 157409,	c 785	17	0.8	635	4	US-09-270-767-18724	Sequence 18724, A
c 713	17	0.8	601	4	US-09-949-016-157515	Sequence 157515,	c 786	17	0.8	667	4	US-09-270-767-5146	Sequence 5146, Ap
c 714	17	0.8	601	4	US-09-949-016-157516	Sequence 157516,	c 787	17	0.8	667	4	US-09-270-767-20428	Sequence 20428, A
c 715	17	0.8	601	4	US-09-949-016-158573	Sequence 158573,	c 788	17	0.8	691	4	US-09-799-451-437	Sequence 437, App
716	17	0.8	601	4	US-09-949-016-161273	Sequence 161273,	c 789	17	0.8	694	4	US-09-270-767-6951	Sequence 6951, Ap
c 717	17	0.8	601	4	US-09-949-016-161952	Sequence 161952,	c 790	17	0.8	694	4	US-09-270-767-22233	Sequence 22233, A
c 718	17	0.8	601	4	US-09-949-016-161953	Sequence 161953,	c 791	17	0.8	700	3	US-08-998-416-302	Sequence 302, App
719	17	0.8	601	4	US-09-949-016-162397	Sequence 162397,	c 792	17	0.8	705	3	US-09-328-111-674	Sequence 674, App
c 720	17	0.8	601	4	US-09-949-016-162992	Sequence 162992,	c 793	17	0.8	714	3	US-08-998-416-863	Sequence 863, App
c 721	17	0.8	601	4	US-09-949-016-163027	Sequence 163027,	c 794	17	0.8	714	3	US-08-998-416-1139	Sequence 1139, Ap
c 722	17	0.8	601	4	US-09-949-016-163028	Sequence 163028,	c 795	17	0.8	722	3	US-08-998-416-680	Sequence 680, App
c 723	17	0.8	601	4	US-09-949-016-163120	Sequence 163120,	c 796	17	0.8	725	3	US-08-998-416-1051	Sequence 1051, Ap
c 724	17	0.8	601	4	US-09-949-016-163137	Sequence 163137,	c 797	17	0.8	732	4	US-09-248-796A-1557	Sequence 1557, Ap
c 725	17	0.8	601	4	US-09-949-016-163138	Sequence 163138,	c 798	17	0.8	761	3	US-08-998-416-382	Sequence 382, App
c 726	17	0.8	601	4	US-09-949-016-163924	Sequence 163924,	c 799	17	0.8	771	4	US-09-489-039A-6682	Sequence 6682, Ap
c 727	17	0.8	601	4	US-09-949-016-165310	Sequence 165310,	c 800	17	0.8	771	4	US-09-134-000C-2455	Sequence 2455, Ap
c 728	17	0.8	601	4	US-09-949-016-166280	Sequence 166280,	c 801	17	0.8	810	4	US-09-270-767-23360	Sequence 23360, A
c 729	17	0.8	601	4	US-09-949-016-169126	Sequence 169126,	c 802	17	0.8	812	4	US-09-270-767-10727	Sequence 10727, A
730	17	0.8	601	4	US-09-949-016-171844	Sequence 171844,	c 803	17	0.8	822	3	US-09-651-656-8	Sequence 8, Appli
c 731	17	0.8	601	4	US-09-949-016-171845	Sequence 171845,	c 804	17	0.8	825	3	US-09-650-855-8	Sequence 14, Appl
c 732	17	0.8	601	4	US-09-949-016-171847	Sequence 171847,	c 805	17	0.8	848	4	US-09-248-796A-6013	Sequence 6013, Ap
c 733	17	0.8	601	4	US-09-949-016-171848	Sequence 171848,	c 806	17	0.8	848	4	US-09-509-712B-14	Sequence 14, Appl
c 734	17	0.8	601	4	US-09-949-016-172949	Sequence 172949,	c 807	17	0.8	886	4	US-09-270-767-23354	Sequence 25354, A
c 735	17	0.8	601	4	US-09-949-016-173974	Sequence 173974,	c 808	17	0.8	917	4	US-09-270-767-25085	Sequence 28085, A
c 736	17	0.8	601	4	US-09-949-016-173976	Sequence 173976,	c 809	17	0.8	918	4	US-09-248-796A-1982	Sequence 1982, Ap
c 737	17	0.8	601	4	US-09-949-016-173977	Sequence 173977,	c 810	17	0.8	927	4	US-09-976-594-440	Sequence 440, App
c 738	17	0.8	601	4	US-09-949-016-173978	Sequence 173978,	c 811	17	0.8	950	4	US-08-958-009D-8	Sequence 8, Appli
739	17	0.8	601	4	US-09-949-016-17496	Sequence 17496,	c 812	17	0.8	950	4	US-08-958-009D-15	Sequence 15, Appl
c 740	17	0.8	601	4	US-09-949-016-175498	Sequence 175498,	c 813	17	0.8	1158	4	US-09-248-796A-2507	Sequence 2507, Ap
c 741	17	0.8	601	4	US-09-949-016-177418	Sequence 177418,	c 814	17	0.8	1167	4	US-09-663-600A-441	Sequence 141, App
742	17	0.8	601	4	US-09-949-016-178223	Sequence 178223,	c 815	17	0.8	1196	4	US-09-270-767-5074	Sequence 5074, Ap
743	17	0.8	601	4	US-09-949-016-178752	Sequence 178752,	c 816	17	0.8	1196	4	US-09-270-767-20356	Sequence 20356, A
c 744	17	0.8	601	4	US-09-949-016-182541	Sequence 182541,	c 817	17	0.8	1205	4	US-09-401-064-123	Sequence 123, App
c 745	17	0.8	601	4	US-09-949-016-182542	Sequence 182542,	c 818	17	0.8	1220	2	US-08-940-767-3	Sequence 3, Appli
c 746	17	0.8	601	4	US-09-949-016-182552	Sequence 182552,	c 819	17	0.8	1220	3	US-08-941-155-3	Sequence 3, Appli
c 747	17	0.8	601	4	US-09-949-016-182661	Sequence 182661,	c 820	17	0.8	1220	3	US-09-344-686-3	Sequence 3, Appli
c 748	17	0.8	601	4	US-09-949-016-182662	Sequence 182662,	c 821	17	0.8	1220	3	US-09-872-047-3	Sequence 3, Appli
c 749	17	0.8	601	4	US-09-949-016-182672	Sequence 182672,	c 822	17	0.8	1246	4	US-09-866-108A-15706	Sequence 15706, A
750	17	0.8	601	4	US-09-949-016-183236	Sequence 183236,	c 823	17	0.8	1274	4	US-09-148-545-72	Sequence 72, Appl
751	17	0.8	601	4	US-09-949-016-183237	Sequence 183237,	c 824	17	0.8	1276	3	US-09-177-325-2	Sequence 2, Appli
c 752	17	0.8	601	4	US-09-949-016-183238	Sequence 183238,	c 825	17	0.8	1276	3	US-09-411-812A-2	Sequence 2, Appli
c 753	17	0.8	601	4	US-09-949-016-183676	Sequence 183676,	c 826	17	0.8	1276	3	US-09-590-113-2	Sequence 2, Appli
c 754	17	0.8	601	4	US-09-949-016-183863	Sequence 183863,	c 827	17	0.8	1278	4	US-09-583-110-1754	Sequence 1754, Ap
c 755	17	0.8	601	4	US-09-949-016-184739	Sequence 184739,	c 828	17	0.8	1287	4	US-09-107-433-2170	Sequence 2170, Ap
c 756	17	0.8	601	4	US-09-949-016-185536	Sequence 185536,	c 829	17	0.8	1296	4	US-09-134-000C-1947	Sequence 1947, Ap
c 757	17	0.8	601	4	US-09-949-016-185623	Sequence 185623,	c 830	17	0.8	1305	6	5212087-1	Patent No. 5212087

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C 832	17	0.8	1370	4	US-09-663-600A-47	Sequence 47, Appl	905	17	0.8	2474	4	US-09-270-767-10028	Sequence 10028, A
C 833	17	0.8	1377	4	US-09-949-016-3717	Sequence 3717, Ap	C 906	17	0.8	2508	4	US-09-949-016-2289	Sequence 2289, Ap
C 834	17	0.8	1384	4	US-09-461-325-24	Sequence 24, Appl	C 907	17	0.8	2552	4	US-09-270-767-15247	Sequence 15247, A
C 835	17	0.8	1384	4	US-10-012-542-24	Sequence 24, Appl	C 908	17	0.8	2582	4	US-09-480-017-3	Sequence 3, Appl
C 836	17	0.8	1384	4	US-10-115-123-24	Sequence 24, Appl	C 909	17	0.8	2588	3	US-09-543-684A-1162	Sequence 1162, Ap
C 837	17	0.8	1398	4	US-09-710-279-1675	Sequence 1675, Ap	C 910	17	0.8	2754	4	US-09-248-796A-4857	Sequence 4857, Ap
C 838	17	0.8	1421	4	US-09-270-767-12333	Sequence 12333, A	C 911	17	0.8	2760	4	US-09-248-796A-1053	Sequence 1053, Ap
C 839	17	0.8	1422	4	US-08-248-796A-1981	Sequence 1981, Ap	C 912	17	0.8	2782	4	US-09-134-001C-4372	Sequence 4372, Ap
C 840	17	0.8	1426	4	US-09-620-312B-967	Sequence 967, App	C 913	17	0.8	2797	4	US-09-949-016-376	Sequence 376, App
C 841	17	0.8	1443	4	US-09-270-767-13193	Sequence 13193, A	C 914	17	0.8	2848	3	US-08-539-205A-3	Sequence 3, Appl
C 842	17	0.8	1455	3	US-09-134-001C-2226	Sequence 2226, Ap	C 915	17	0.8	2848	4	US-09-392-163A-3	Sequence 3, Appl
C 843	17	0.8	1457	4	US-09-638-937-1	Sequence 1, Appl	C 916	17	0.8	2848	4	US-09-392-163A-3	Sequence 3, Appl
C 844	17	0.8	1467	4	US-09-949-016-2761	Sequence 2761, Ap	C 917	17	0.8	2862	4	US-09-499-203-13	Sequence 13, Appl
C 845	17	0.8	1484	4	US-08-956-171B-595	Sequence 595, App	C 918	17	0.8	2839	4	US-09-270-767-26336	Sequence 26336, A
C 846	17	0.8	1484	4	US-08-781-986A-595	Sequence 595, App	C 919	17	0.8	2973	1	US-08-451-715A-7	Sequence 7, Appl
C 847	17	0.8	1499	4	US-09-023-655-80	Sequence 80, Appl	C 920	17	0.8	2976	4	US-09-386-963C-7	Sequence 7, Appl
C 848	17	0.8	1500	3	US-09-593-711A-10	Sequence 10, Appl	C 921	17	0.8	2976	4	US-09-386-963C-7	Sequence 7, Appl
C 849	17	0.8	1647	4	US-09-248-796A-406	Sequence 406, App	C 922	17	0.8	3001	4	US-09-539-333D-205	Sequence 205, App
C 850	17	0.8	1666	4	US-09-799-451-479	Sequence 479, App	C 923	17	0.8	3007	4	US-09-710-279-3846	Sequence 3846, Ap
C 851	17	0.8	1688	4	US-09-270-767-31585	Sequence 31585, A	C 924	17	0.8	3020	4	US-09-220-132-19	Sequence 19, Appl
C 852	17	0.8	1698	4	US-09-861-451A-31	Sequence 31, Appl	C 925	17	0.8	3090	4	US-09-710-279-3599	Sequence 3599, Ap
C 853	17	0.8	1700	1	US-08-539-304A-3	Sequence 3, Appl	C 926	17	0.8	3100	3	US-08-936-165A-184	Sequence 184, App
C 854	17	0.8	1710	3	US-09-134-001C-2735	Sequence 2735, Ap	C 927	17	0.8	3304	4	US-09-710-279-3740	Sequence 3740, Ap
C 855	17	0.8	1728	4	US-09-614-221A-461	Sequence 461, App	C 928	17	0.8	3467	3	US-09-298-924-3	Sequence 3, Appl
C 856	17	0.8	1731	3	US-09-149-476-277	Sequence 277, App	C 929	17	0.8	3467	4	US-09-743-492A-1	Sequence 1, Appl
C 857	17	0.8	1746	4	US-08-147-405B-12	Sequence 12, Appl	C 930	17	0.8	3477	4	US-09-513-505-10	Sequence 10, Appl
C 858	17	0.8	1747	4	US-08-956-171B-685	Sequence 685, App	C 931	17	0.8	3585	4	US-09-270-767-14479	Sequence 14, Appl
C 859	17	0.8	1747	4	US-08-781-986A-685	Sequence 685, App	C 932	17	0.8	3600	4	US-09-147-405B-14	Sequence 14, Appl
C 860	17	0.8	1760	1	US-08-413-118-117	Sequence 117, App	C 933	17	0.8	3741	4	PCT-US95-13749-1	Sequence 10858, A
C 861	17	0.8	1760	3	US-08-473-446-117	Sequence 117, Appl	C 934	17	0.8	3741	4	US-09-270-767-10858	Sequence 28, Appl
C 862	17	0.8	1781	4	US-09-147-405B-10	Sequence 10, Appl	C 935	17	0.8	3816	4	US-09-710-279-4214	Sequence 28, Appl
C 863	17	0.8	1788	4	US-09-248-796A-459	Sequence 459, App	C 936	17	0.8	3898	5	US-08-471-791-28	Sequence 1, Appl
C 864	17	0.8	1821	4	US-09-205-258-43	Sequence 43, Appl	C 937	17	0.8	3928	2	PCT-US91-01746-28	Sequence 1, Appl
C 865	17	0.8	1830	2	US-08-933-750C-79	Sequence 79, Appl	C 938	17	0.8	3928	2	US-08-731-722-1	Sequence 1, Appl
C 866	17	0.8	1830	3	US-09-234-613-79	Sequence 79, Appl	C 939	17	0.8	3926	2	US-08-731-722-1	Sequence 2, Appl
C 867	17	0.8	1858	4	US-09-270-767-10460	Sequence 10460, A	C 940	17	0.8	3926	2	US-08-731-722-2	Sequence 2, Appl
C 868	17	0.8	1864	3	US-09-149-476-130	Sequence 130, App	C 941	17	0.8	3933	2	US-08-731-722-2	Sequence 3, Appl
C 869	17	0.8	1876	3	US-08-714-318-33	Sequence 33, Appl	C 942	17	0.8	3933	2	US-08-731-722-3	Sequence 3, Appl
C 870	17	0.8	1876	3	US-09-265-315-33	Sequence 33, Appl	C 943	17	0.8	4073	3	US-09-270-767-13399	Sequence 13399, A
C 871	17	0.8	1876	3	US-09-265-315-33	Sequence 33, Appl	C 944	17	0.8	4422	3	US-09-166-350-1	Sequence 1, Appl
C 872	17	0.8	1876	3	US-09-266-417-33	Sequence 33, Appl	C 945	17	0.8	4422	3	US-09-949-016-13991	Sequence 1, Appl
C 873	17	0.8	1876	4	US-09-528-709-33	Sequence 33, Appl	C 946	17	0.8	4550	4	US-09-331-581-1	Sequence 5, Appl
C 874	17	0.8	1876	4	US-09-527-745-33	Sequence 33, Appl	C 947	17	0.8	4748	3	US-09-866-108A-5	Sequence 14874, A
C 875	17	0.8	1908	2	US-08-909-565C-17	Sequence 17, Appl	C 948	17	0.8	4916	4	US-09-949-016-14874	Sequence 241, App
C 876	17	0.8	1919	4	US-09-949-016-220	Sequence 220, App	C 949	17	0.8	4982	4	US-08-556-171B-241	Sequence 241, App
C 877	17	0.8	1921	4	US-09-949-016-2094	Sequence 2094, Ap	C 950	17	0.8	5000	4	US-08-781-986A-241	Sequence 100, App
C 878	17	0.8	1931	4	US-09-976-594-329	Sequence 329, App	C 951	17	0.8	5075	4	US-09-949-016-100	Sequence 100, App
C 879	17	0.8	1977	4	US-08-705-477E-99	Sequence 99, Appl	C 952	17	0.8	5075	4	US-09-949-016-100	Sequence 100, App
C 880	17	0.8	2056	4	US-09-498-557-20	Sequence 20, Appl	C 953	17	0.8	5089	6	5177197-31	Patent No. 5177197
C 881	17	0.8	2081	3	US-09-149-476-123	Sequence 123, App	C 954	17	0.8	5089	6	5177197-31	Patent No. 5177197
C 882	17	0.8	2099	4	US-09-949-016-2191	Sequence 2191, Ap	C 955	17	0.8	5310	4	US-09-620-312D-623	Sequence 623, App
C 883	17	0.8	2160	2	US-08-840-236-2	Sequence 2, Appl	C 956	17	0.8	5449	4	US-09-949-016-2138	Sequence 2138, Ap
C 884	17	0.8	2160	2	US-08-840-236-5	Sequence 5, Appl	C 957	17	0.8	5516	4	US-09-949-016-868	Sequence 868, App
C 885	17	0.8	2160	2	US-08-505-448A-2	Sequence 2, Appl	C 958	17	0.8	5605	3	US-09-268-140-6	Sequence 6, Appl
C 886	17	0.8	2160	2	US-08-505-448A-5	Sequence 5, Appl	C 959	17	0.8	5749	4	US-09-949-016-15441	Sequence 15441, A
C 887	17	0.8	2169	4	US-09-976-594-315	Sequence 315, App	C 960	17	0.8	5749	4	US-09-949-016-15442	Sequence 15442, A
C 888	17	0.8	2223	1	US-08-257-073-4	Sequence 4, Appl	C 961	17	0.8	5819	3	US-09-949-016-16028	Sequence 16028, A
C 889	17	0.8	2268	3	US-08-873-093-2	Sequence 2, Appl	C 962	17	0.8	5819	3	US-08-987-123-4	Sequence 4, Appl
C 890	17	0.8	2268	3	US-09-206-646-2	Sequence 2, Appl	C 963	17	0.8	6002	4	US-09-590-211A-18	Sequence 18, Appl
C 891	17	0.8	2280	1	US-08-220-151-11	Sequence 11, Appl	C 964	17	0.8	6027	4	US-09-620-312D-517	Sequence 517, App
C 892	17	0.8	2280	1	US-08-413-118-11	Sequence 11, Appl	C 965	17	0.8	6043	4	US-09-989-981A-9	Sequence 9, Appl
C 893	17	0.8	2280	3	US-08-473-446-11	Sequence 11, Appl	C 966	17	0.8	6055	4	US-09-953-318-10	Sequence 10, Appl
C 894	17	0.8	2287	4	US-09-561-763-7	Sequence 7, Appl	C 967	17	0.8	6204	3	US-09-499-203-20	Sequence 20, Appl
C 895	17	0.8	2287	4	US-09-431-367B-7	Sequence 7, Appl	C 968	17	0.8	6216	3	US-09-213-053-1	Sequence 1, Appl
C 896	17	0.8	2315	3	US-08-961-527-194	Sequence 194, App	C 969	17	0.8	6305	3	US-08-687-580B-6	Sequence 6, Appl
C 897	17	0.8	2331	4	US-09-866-028-54	Sequence 54, Appl	C 970	17	0.8	6356	4	US-09-770-595A-1	Sequence 1, Appl
C 898	17	0.8	2331	4	US-09-944-457-54	Sequence 54, Appl	C 971	17	0.8	6908	4	US-09-949-016-14842	Sequence 14842, A
C 899	17	0.8	2335	2	US-08-300-584-3	Sequence 3, Appl	C 972	17	0.8	7173	4	US-09-949-016-17491	Sequence 17491, A
C 900	17	0.8	2335	3	US-08-476-123-3	Sequence 3, Appl	C 973	17	0.8	7244	3	US-08-378-313-26	Sequence 26, Appl
C 901	17	0.8	2335	3	US-09-742-684A-3	Sequence 3, Appl	C 974	17	0.8	7286	3	US-09-331-581-3	Sequence 3, Appl
C 902	17	0.8	2368	4	US-09-270-767-9834	Sequence 9834, Ap	C 975	17	0.8	7387	4	US-09-499-203-17	Sequence 17, Appl
C 903	17	0.8	2409	3	US-09-484-970B-101	Sequence 101, App	C 976	17	0.8	7424	4	US-09-949-016-13898	Sequence 13898, A

977 17 0.8 7702 4 US-09-023-655-1336 Sequence 1336, Ap
978 17 0.8 7702 4 US-09-743-492A-3 Sequence 3, Appli
C 979 17 0.8 7707 4 US-09-866-108A-2 Sequence 2, Appli
C 980 17 0.8 7716 4 US-09-949-016-16614 Sequence 16614, A
981 17 0.8 7938 3 US-09-331-581-14 Sequence 14, Appli
C 982 17 0.8 8117 4 US-09-866-108A-1 Sequence 1, Appli
983 17 0.8 8205 4 US-09-949-016-1500 Sequence 1500, Ap
984 17 0.8 8220 4 US-09-949-016-932 Sequence 932, App
985 17 0.8 8405 4 US-09-949-016-11882 Sequence 11882, A
986 17 0.8 8405 4 US-09-949-016-15376 Sequence 15376, A
987 17 0.8 8641 4 US-09-949-016-14077 Sequence 14077, A
C 988 17 0.8 8658 4 US-09-949-016-17038 Sequence 17038, A
C 989 17 0.8 9098 4 US-09-358-082A-28 Sequence 28, Appl
C 990 17 0.8 9098 4 US-09-358-082A-28 Sequence 28, Appl
991 17 0.8 9169 4 US-09-949-016-11948 Sequence 11948, A
992 17 0.8 9170 4 US-09-949-016-17079 Sequence 17079, A
993 17 0.8 9321 4 US-09-499-203-1 Sequence 1, Appli
C 994 17 0.8 9406 4 US-09-949-016-17494 Sequence 17494, A
C 995 17 0.8 9527 4 US-09-949-016-13979 Sequence 13979, A
996 17 0.8 9884 4 US-09-949-016-12548 Sequence 12548, A
997 17 0.8 9889 4 US-09-949-016-16116 Sequence 16116, A
C 998 17 0.8 10160 4 US-09-949-016-13215 Sequence 13215, A
C 999 17 0.8 10207 1 US-08-920-812-2 Sequence 2, Appli
C1000 17 0.8 10207 1 US-08-920-827-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-961-527-80/c
; Sequence 80, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-80
Query Match 1.1%; Score 22; DB 3; Length 9607;
Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 TTCTCTTTCTTTCTTTTATTT 53
Db 8125 TTCTCTTTCTTTCTTTTATTT 8104
RESULT 2
US-09-142-569-5/c
; Sequence 5, Application US/09142569
; Patent No. 6413735
; GENERAL INFORMATION:
; APPLICANT: Lau, Lester F.
; TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,569
; FILING DATE: 02-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28758/33766
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2267 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Fisp12 cDNA coding sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-569-5
Query Match 1.0%; Score 21; DB 3; Length 2267;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 199 TTTTCATATAAAATATATA 219
Db 2256 TTTTCATATAAAATATATA 2236
RESULT 3
US-09-495-448A-5/c
; Sequence 5, Application US/09495448A
; Patent No. 6790606
; GENERAL INFORMATION:
; APPLICANT: Lau, Lester F.
; TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES
; FILE REFERENCE: 28758/36072 US/09/495,448A
; CURRENT APPLICATION NUMBER: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/142,569
; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: 60/013,958
; PRIOR FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Fisp12 cDNA coding sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (138)..(1181)
US-09-495-448A-5

Query Match 1.0%; Score 21; DB 4; Length 2267;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAAAATATATA 219
|||||
Db 2256 TTTTCATATAAAAAATATATA 2236

RESULT 4
US-09-582-337-1/c
; Sequence 1, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(212)
; NAME/KEY: CDS
; LOCATION: (213)..(1256)
; NAME/KEY: 3'UTR
; LOCATION: (1257)..(2338)
; NAME/KEY: polyA signal
; LOCATION: (2297)..(2302)
US-09-582-337-1

Query Match 1.0%; Score 21; DB 4; Length 2338;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAAAATATATA 219
|||||
Db 2326 TTTTCATATAAAAAATATATA 2306

RESULT 5
US-09-187-478-1/c
; Sequence 1, Application US/09187478
; Patent No. 6348329
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Brian F.
; APPLICANT: Allen, Margaret L.
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use

; FILE REFERENCE: 08766/004001
; CURRENT APPLICATION NUMBER: US/09/187,478
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-187-478-1

Query Match 1.0%; Score 21; DB 3; Length 2350;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAAAATATATA 219
|||||
Db 2328 TTTTCATATAAAAAATATATA 2308

RESULT 6
US-09-292-036-1/c
; Sequence 1, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIBRO100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-292-036-1

Query Match 1.0%; Score 21; DB 3; Length 2350;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAAAATATATA 219
|||||
Db 2328 TTTTCATATAAAAAATATATA 2308

RESULT 7
US-09-949-016-11751/c
; Sequence 11751, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11751
; LENGTH: 40742
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11751

Query Match 1.0%; Score 21; DB 4; Length 40742;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 ATTACAAAAGGAAAAA 93
Db 38117 ATTACAAAAGGAAAAA 38097

RESULT 8
US-09-949-016-13097/c
; Sequence 13097, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13097
; LENGTH: 40747
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13097

Query Match 1.0%; Score 21; DB 4; Length 40747;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 ATTACAAAAGGAAAAA 93
Db 38117 ATTACAAAAGGAAAAA 38097

RESULT 9
US-09-823-634A-13
; Sequence 13, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match 1.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1591 AAAAAAAATTTGAAAAA 1610
Db 1 AAAAAAAATTTGAAAAA 20

RESULT 10
US-09-823-647B-13
; Sequence 13, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match 1.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1591 AAAAAAAATTTGAAAAA 1610
Db 1 AAAAAAAATTTGAAAAA 20

RESULT 11
US-09-248-796A-8498/c
; Sequence 8498, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8498
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (156)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-248-796A-8498

Query Match 1.0%; Score 20; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 AAAAGGAAAAAATAAT 97
Db 138 AAAAGGAAAAAATAAT 119

RESULT 12
US-09-601-198-173
; Sequence 173, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-173

Query Match 1.0%; Score 20; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1969 GTTTATTAAATTGACAGATT 1988
Db 138 GTTTATTAAATTGACAGATT 157

RESULT 13
US-09-786-454A-1
; Sequence 1, Application US/09786454A
; Patent No. 6589532
; GENERAL INFORMATION:
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: PAPILLOMA VIRUSES, MEANS FOR THE DETECTION THEREOF AND THERAPY FOR
; FILE REFERENCE: 8484-097-999
; CURRENT APPLICATION NUMBER: US/09/786,454A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Papillomavirus sylvilagi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(423)
US-09-786-454A-1

Query Match 1.0%; Score 20; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 AATTTTACTATTGTACCGC 899
|||||

Db 43 AATTTTACTATTGTACCGC 62

RESULT 14

US-09-949-016-28079
; Sequence 28079, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28079
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-28079

Query Match 1.0%; Score 20; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TTTTCTATTTTTATTGATT 57
Db 215 TTTTCTATTTTTATTGATT 234

RESULT 15

US-09-949-016-42035/c
; Sequence 42035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42035
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-42035

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Search completed: October 24, 2005, 06:43:30
Job time : 905 secs

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C 84	20	1.0	439	12	US-09-925-065A-217402	Sequence 217402,	C 157	20	1.0	5158	17	US-10-275-933-11	Sequence 11, Appl
C 85	20	1.0	440	12	US-09-925-065A-478249	Sequence 478249,	C 158	20	1.0	5571	17	US-10-221-613-202	Sequence 202, App
C 86	20	1.0	464	12	US-09-925-065A-829462	Sequence 829462,	C 159	20	1.0	5571	18	US-10-221-714A-206	Sequence 206, App
C 87	20	1.0	470	18	US-10-424-599-48845	Sequence 48845, A	C 160	20	1.0	5986	15	US-10-240-453-272	Sequence 272, App
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C 104	20	1.0	572	17	US-10-027-632-220249	Sequence 220249,	C 177	20	1.0	117754	13	US-10-087-192-28	Sequence 28, Appl
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279	19	0.9	565	12	US-09-925-065A-652893	Sequence 652893, A	C 352	19	0.9	631	21	US-09-925-065A-875150	Sequence 875150,
280	19	0.9	566	20	US-10-357-930-51743	Sequence 51743, A	C 353	19	0.9	636	12	US-09-925-065A-81491	Sequence 81491, A
281	19	0.9	568	12	US-09-925-065A-319480	Sequence 319480, A	C 354	19	0.9	636	12	US-09-925-065A-81492	Sequence 81492, A
282	19	0.9	568	12	US-09-925-065A-319481	Sequence 319481, A	C 355	19	0.9	636	12	US-09-925-065A-116798	Sequence 116798,
283	19	0.9	569	12	US-09-925-065A-436614	Sequence 436614, A	C 356	19	0.9	636	12	US-09-925-065A-525225	Sequence 525225,
284	19	0.9	571	12	US-09-925-065A-933026	Sequence 933026, A	C 357	19	0.9	639	12	US-09-925-065A-525226	Sequence 525226,
285	19	0.9	572	12	US-09-925-065A-426657	Sequence 426657, A	C 358	19	0.9	639	12	US-09-925-065A-525228	Sequence 525228,
286	19	0.9	573	12	US-09-925-065A-446871	Sequence 446871, A	C 359	19	0.9	639	12	US-09-925-065A-525229	Sequence 525229,
287	19	0.9	577	12	US-09-925-065A-762693	Sequence 762693, A	C 360	19	0.9	640	12	US-09-925-065A-682741	Sequence 682741,
288	19	0.9	577	20	US-10-425-115-171050	Sequence 171050, A	C 361	19	0.9	640	12	US-09-925-065A-682742	Sequence 682742,
289	19	0.9	578	12	US-09-925-065A-823498	Sequence 823498, A	C 362	19	0.9	640	12	US-09-925-065A-682743	Sequence 682743,
290	19	0.9	578	16	US-10-029-386-6290	Sequence 6290, Ap	C 363	19	0.9	640	12	US-09-925-065A-74233	Sequence 74233, A
291	19	0.9	579	12	US-09-925-065A-656786	Sequence 656786, A	C 364	19	0.9	647	12	US-10-437-963-74233	Sequence 74233, A
292	19	0.9	580	12	US-09-925-065A-410834	Sequence 410834, A	C 365	19	0.9	656	12	US-09-925-065A-413343	Sequence 413343,
293	19	0.9	580	12	US-09-925-065A-410836	Sequence 410836, A	C 366	19	0.9	656	12	US-09-925-065A-413344	Sequence 413344,
294	19	0.9	582	12	US-09-925-065A-439092	Sequence 439092, A	C 367	19	0.9	658	12	US-09-925-065A-5440	Sequence 5440, Ap
295	19	0.9	584	12	US-09-925-065A-574172	Sequence 574172, A	C 368	19	0.9	661	13	US-09-925-065A-914163	Sequence 914163,
296	19	0.9	585	12	US-09-925-065A-267914	Sequence 267914, A	C 369	19	0.9	664	13	US-10-027-632-7741	Sequence 7741, Ap
297	19	0.9	585	12	US-09-925-065A-267916	Sequence 267916, A	C 370	19	0.9	664	17	US-10-027-632-7741	Sequence 7741, Ap
298	19	0.9	585	13	US-10-027-632-248035	Sequence 248035, A	C 371	19	0.9	670	13	US-10-027-632-170985	Sequence 170985,
299	19	0.9	585	17	US-10-027-632-248035	Sequence 248035, A	C 372	19	0.9	670	17	US-10-027-632-170985	Sequence 170985,

373	19	0.9	696	12	US-09-925-065A-947173	Sequence 947173, A	19	0.9	1630	12	US-09-925-065A-711468	Sequence 711468, A
c 374	19	0.9	696	14	US-10-198-846-12804	Sequence 12804, A	19	0.9	1665	20	US-10-425-115-49808	Sequence 49808, A
375	19	0.9	702	13	US-10-027-632-159391	Sequence 159391, A	19	0.9	1666	22	US-10-491-355-41	Sequence 41, Appl
376	19	0.9	702	13	US-10-027-632-159392	Sequence 159392, A	19	0.9	1764	12	US-09-925-065A-696442	Sequence 696442, A
377	19	0.9	702	17	US-10-027-632-159391	Sequence 159391, A	19	0.9	1764	12	US-09-925-065A-696443	Sequence 696443, A
378	19	0.9	702	17	US-10-027-632-159392	Sequence 159392, A	19	0.9	1782	18	US-10-149-310-81	Sequence 81, Appl
c 379	19	0.9	705	12	US-09-925-065A-75401	Sequence 75401, A	19	0.9	1803	9	US-09-956-004-71	Sequence 71, Appl
c 380	19	0.9	705	12	US-09-925-065A-75402	Sequence 75402, A	19	0.9	1803	9	US-10-808-570-71	Sequence 6, Appl
381	19	0.9	705	12	US-09-925-065A-3486	Sequence 3486, A	19	0.9	1821	9	US-09-737-178-6	Sequence 6, Appl
382	19	0.9	736	17	US-10-027-632-149323	Sequence 149323, A	19	0.9	1821	9	US-09-286-488-6	Sequence 6, Appl
383	19	0.9	736	17	US-10-027-632-149323	Sequence 149323, A	19	0.9	1821	10	US-09-853-079-6	Sequence 6, Appl
384	19	0.9	746	17	US-10-027-632-164736	Sequence 164736, A	19	0.9	1821	17	US-10-294-443-6	Sequence 6, Appl
385	19	0.9	746	17	US-10-027-632-164736	Sequence 164736, A	19	0.9	1821	17	US-10-294-443-6	Sequence 6, Appl
386	19	0.9	751	13	US-10-027-632-98953	Sequence 98953, A	19	0.9	1868	11	US-09-938-842A-5068	Sequence 5068, A
387	19	0.9	751	13	US-10-027-632-98953	Sequence 98953, A	19	0.9	1868	11	US-09-938-842A-5068	Sequence 5068, A
388	19	0.9	762	17	US-10-027-632-151185	Sequence 151185, A	19	0.9	1934	14	US-09-925-065A-680444	Sequence 680444, A
389	19	0.9	762	17	US-10-027-632-151185	Sequence 151185, A	19	0.9	2135	14	US-10-234-432-16	Sequence 16, Appl
390	19	0.9	767	20	US-10-363-345A-8369	Sequence 8369, A	19	0.9	2639	24	US-11-097-143-1190	Sequence 1190, A
c 391	19	0.9	767	20	US-10-363-345A-8370	Sequence 8370, A	19	0.9	2726	17	US-10-104-047-877	Sequence 877, A
392	19	0.9	767	21	US-10-363-483A-8369	Sequence 8369, A	19	0.9	3107	15	US-10-172-086-94	Sequence 94, Appl
c 393	19	0.9	767	21	US-10-363-483A-8370	Sequence 8370, A	19	0.9	3107	15	US-10-172-086-94	Sequence 94, Appl
394	19	0.9	789	13	US-10-027-632-168159	Sequence 168159, A	19	0.9	3107	15	US-10-311-507-82	Sequence 82, Appl
395	19	0.9	789	13	US-10-027-632-168159	Sequence 168159, A	19	0.9	3374	24	US-10-104-047-877	Sequence 877, A
396	19	0.9	789	17	US-10-027-632-168159	Sequence 168159, A	19	0.9	3374	24	US-10-104-047-877	Sequence 877, A
397	19	0.9	789	17	US-10-027-632-168159	Sequence 168159, A	19	0.9	3948	18	US-10-302-172-125	Sequence 125, A
c 398	19	0.9	794	19	US-10-027-632-168160	Sequence 168160, A	19	0.9	4223	9	US-09-737-178-7	Sequence 7, Appl
399	19	0.9	810	20	US-10-425-115-124194	Sequence 124194, A	19	0.9	4223	9	US-09-737-178-7	Sequence 7, Appl
c 400	19	0.9	812	13	US-10-027-632-152589	Sequence 152589, A	19	0.9	4223	9	US-09-286-488-7	Sequence 7, Appl
c 401	19	0.9	812	13	US-10-027-632-152589	Sequence 152589, A	19	0.9	4223	10	US-09-286-488-7	Sequence 7, Appl
c 402	19	0.9	812	13	US-10-027-632-152591	Sequence 152591, A	19	0.9	4223	10	US-09-853-079-7	Sequence 7, Appl
c 403	19	0.9	812	17	US-10-027-632-152589	Sequence 152589, A	19	0.9	4223	10	US-09-853-079-7	Sequence 7, Appl
c 404	19	0.9	812	17	US-10-027-632-152590	Sequence 152590, A	19	0.9	4223	17	US-10-294-443-7	Sequence 7, Appl
c 405	19	0.9	812	17	US-10-027-632-152591	Sequence 152591, A	19	0.9	4223	17	US-10-294-443-7	Sequence 7, Appl
406	19	0.9	856	24	US-10-425-114-6864	Sequence 6864, A	19	0.9	4223	17	US-10-294-443-45	Sequence 45, Appl
c 407	19	0.9	856	24	US-10-425-114-6864	Sequence 6864, A	19	0.9	4223	17	US-10-294-443-45	Sequence 45, Appl
c 408	19	0.9	879	18	US-10-424-599-94162	Sequence 94162, A	19	0.9	4945	24	US-11-037-143-1189	Sequence 1189, A
c 409	19	0.9	879	20	US-10-425-115-173241	Sequence 173241, A	19	0.9	5129	19	US-10-788-752-25	Sequence 25, Appl
c 410	19	0.9	899	19	US-10-437-963-27088	Sequence 27088, A	19	0.9	5338	17	US-10-221-613-242	Sequence 242, A
c 411	19	0.9	930	22	US-10-724-972A-3583	Sequence 3583, A	19	0.9	5442	15	US-10-311-455-1941	Sequence 1941, A
412	19	0.9	949	20	US-10-425-115-16816	Sequence 16816, A	19	0.9	5569	24	US-11-097-143-12787	Sequence 12787, A
c 413	19	0.9	987	17	US-10-027-632-325426	Sequence 325426, A	19	0.9	5807	15	US-10-311-455-1127	Sequence 1127, A
c 414	19	0.9	987	17	US-10-027-632-325426	Sequence 325426, A	19	0.9	6047	15	US-10-311-455-1432	Sequence 1432, A
c 415	19	0.9	1002	18	US-10-425-114-13976	Sequence 12976, A	19	0.9	6118	15	US-10-311-455-1003	Sequence 1003, A
c 416	19	0.9	1033	9	US-09-778-445-188	Sequence 188, A	19	0.9	6118	15	US-10-311-455-1003	Sequence 1003, A
c 417	19	0.9	1040	14	US-10-278-173-157	Sequence 157, A	19	0.9	6215	15	US-10-311-455-1163	Sequence 1163, A
c 418	19	0.9	1040	15	US-10-278-536-209	Sequence 209, A	19	0.9	6240	15	US-10-311-455-110	Sequence 110, A
c 419	19	0.9	1040	18	US-10-412-699B-341	Sequence 341, A	19	0.9	6240	15	US-10-240-485-8	Sequence 8, Appl
c 420	19	0.9	1044	18	US-10-451-337-7	Sequence 7, Appl	19	0.9	6270	15	US-10-311-455-1846	Sequence 1846, A
c 421	19	0.9	1044	20	US-10-474-792-179	Sequence 179, A	19	0.9	6337	10	US-08-928-847B-49	Sequence 49, Appl
c 422	19	0.9	1078	12	US-09-925-065A-69703	Sequence 69703, A	19	0.9	6866	15	US-10-311-455-640	Sequence 640, A
c 423	19	0.9	1090	20	US-10-425-115-49809	Sequence 49809, A	19	0.9	6988	15	US-10-311-455-2414	Sequence 2414, A
424	19	0.9	1096	18	US-10-424-599-71266	Sequence 71266, A	19	0.9	7058	17	US-10-257-166-133	Sequence 133, A
c 425	19	0.9	1111	16	US-10-252-157-111	Sequence 111, A	19	0.9	7083	24	US-11-097-143-1246	Sequence 1246, A
c 426	19	0.9	1114	13	US-10-027-632-119019	Sequence 119019, A	19	0.9	7222	14	US-10-198-846-13528	Sequence 13528, A
c 427	19	0.9	1114	17	US-10-027-632-119019	Sequence 119019, A	19	0.9	7522	15	US-10-311-455-888	Sequence 888, A
428	19	0.9	1128	13	US-10-027-632-119513	Sequence 119513, A	19	0.9	7544	14	US-10-239-676-6	Sequence 6, Appl
429	19	0.9	1128	17	US-10-027-632-119513	Sequence 119513, A	19	0.9	8103	15	US-10-240-453-14	Sequence 14, A
c 430	19	0.9	1145	13	US-10-027-632-259574	Sequence 259574, A	19	0.9	8168	15	US-10-311-455-1634	Sequence 1634, A
c 431	19	0.9	1145	17	US-10-027-632-259574	Sequence 259574, A	19	0.9	8168	15	US-10-311-455-901	Sequence 901, A
c 432	19	0.9	1172	17	US-10-369-493-29023	Sequence 29023, A	19	0.9	8168	15	US-10-311-455-902	Sequence 902, A
c 433	19	0.9	1253	18	US-10-424-599-37287	Sequence 37287, A	19	0.9	8168	18	US-10-240-454-23	Sequence 23, A
c 434	19	0.9	1283	12	US-09-925-065A-692044	Sequence 692044, A	19	0.9	8530	15	US-10-240-454-24	Sequence 24, A
c 435	19	0.9	1354	20	US-10-425-115-61774	Sequence 61774, A	19	0.9	8758	15	US-10-311-455-405	Sequence 405, A
c 436	19	0.9	1421	12	US-09-925-065A-727205	Sequence 727205, A	19	0.9	8758	15	US-10-311-455-1091	Sequence 1091, A
c 437	19	0.9	1450	19	US-10-437-963-52708	Sequence 52708, A	19	0.9	8915	24	US-11-097-143-1713	Sequence 1713, A
c 438	19	0.9	1451	15	US-10-172-086-63	Sequence 63, Appl	19	0.9	9720	24	US-11-097-143-1713	Sequence 1713, A
c 439	19	0.9	1451	19	US-10-311-507-23	Sequence 23, Appl	19	0.9	9728	15	US-10-311-455-1876	Sequence 1876, A
c 440	19	0.9	1451	20	US-10-480-846-63	Sequence 63, Appl	19	0.9	9914	9	US-09-764-847-1558	Sequence 1558, A
c 441	19	0.9	1470	18	US-10-424-599-66851	Sequence 66851, A	19	0.9	9914	14	US-10-092-154-1558	Sequence 1558, A
c 442	19	0.9	1508	12	US-09-925-065A-698799	Sequence 698799, A	19	0.9	9963	15	US-10-311-455-668	Sequence 668, A
c 443	19	0.9	1559	18	US-10-424-599-21619	Sequence 21619, A	19	0.9	10528	15	US-10-311-455-308	Sequence 308, A
c 444	19	0.9	1581	21	US-10-764-420-2631	Sequence 2631, A	19	0.9	11049	16	US-10-240-589C-30	Sequence 30, A
c 445	19	0.9	1619	18	US-10-424-599-8667	Sequence 8667, A	19	0.9	11670	16	US-10-240-452-25	Sequence 25, Appl
	19	0.9					19	0.9	12816	24	US-11-097-143-28519	Sequence 28519, A
	19	0.9					19	0.9	12986	18	US-10-221-714A-276	Sequence 276, A

C 519	19	0.9	13449	15	US-10-311-455-1358	Sequence 1358, Ap	C 592	19	0.9	168050	22	US-10-939-321-1	Sequence 1, Appl
C 520	19	0.9	14491	20	US-10-473-126-201	Sequence 201, App	C 593	19	0.9	171324	13	US-10-087-192-67	Sequence 67, Appl
C 521	19	0.9	14491	20	US-10-473-126-347	Sequence 347, App	C 594	19	0.9	180227	19	US-10-322-281-308	Sequence 308, App
C 522	19	0.9	15122	15	US-10-311-455-748	Sequence 748, App	C 595	19	0.9	198285	9	US-09-880-107-3814	Sequence 3814, Ap
C 523	19	0.9	15861	15	US-10-311-455-497	Sequence 497, App	C 596	19	0.9	198285	9	US-10-775-169-338	Sequence 338, App
C 524	19	0.9	16127	15	US-10-311-455-718	Sequence 718, App	C 597	19	0.9	198285	22	US-10-756-149-12	Sequence 12, Appl
C 525	19	0.9	16173	15	US-10-240-485-21	Sequence 21, Appl	C 598	19	0.9	203127	21	US-10-741-601-5654	Sequence 5654, Ap
C 526	19	0.9	16688	18	US-10-221-714A-277	Sequence 277, App	C 599	19	0.9	203127	21	US-10-741-600-17666	Sequence 17666, A
C 527	19	0.9	17421	14	US-10-239-676-54	Sequence 54, Appl	C 600	19	0.9	224112	19	US-10-367-094-80	Sequence 80, Appl
C 528	19	0.9	17421	14	US-10-239-676-54	Sequence 54, Appl	C 601	19	0.9	235033	15	US-10-301-844-1	Sequence 1, Appl
C 529	19	0.9	17421	15	US-10-240-453-56	Sequence 56, Appl	C 602	19	0.9	237326	15	US-10-301-844-2	Sequence 2, Appl
C 530	19	0.9	17421	15	US-10-240-453-56	Sequence 56, Appl	C 603	19	0.9	241805	21	US-10-741-601-5621	Sequence 5621, Ap
C 531	19	0.9	17491	15	US-10-240-485-127	Sequence 127, App	C 604	19	0.9	277616	19	US-10-741-600-17581	Sequence 17581, A
C 532	19	0.9	17534	17	US-10-257-166-108	Sequence 108, App	C 605	19	0.9	277616	19	US-10-367-094-83	Sequence 83, Appl
C 533	19	0.9	17721	15	US-10-311-455-1701	Sequence 1701, Ap	C 606	19	0.9	290547	19	US-10-367-094-77	Sequence 77, Appl
C 534	19	0.9	17970	15	US-10-433-793-64	Sequence 64, Appl	C 607	19	0.9	304905	18	US-10-271-416-1	Sequence 1, Appl
C 535	19	0.9	18133	15	US-10-311-455-913	Sequence 913, App	C 608	19	0.9	330973	13	US-10-087-192-1498	Sequence 1498, Ap
C 536	19	0.9	18133	17	US-10-257-166-99	Sequence 99, Appl	C 609	19	0.9	368004	9	US-09-949-654-3	Sequence 3, Appl
C 537	19	0.9	18357	19	US-10-433-793-114	Sequence 114, App	C 610	19	0.9	410846	21	US-10-481-613-1	Sequence 1, Appl
C 538	19	0.9	21500	13	US-10-087-192-169	Sequence 169, App	C 611	19	0.9	580073	16	US-10-205-220-1	Sequence 1, Appl
C 539	19	0.9	25179	19	US-10-322-281-277	Sequence 277, App	C 612	19	0.9	653122	13	US-10-087-192-226	Sequence 226, App
C 540	19	0.9	28118	17	US-10-282-174-402	Sequence 402, App	C 613	19	0.9	653122	14	US-10-067-514-1	Sequence 1, Appl
C 541	19	0.9	28118	17	US-10-282-174-403	Sequence 403, App	C 614	19	0.9	1691139	17	US-10-419-723-1	Sequence 1, Appl
C 542	19	0.9	28118	21	US-10-600-009-402	Sequence 402, App	C 615	19	0.9	1691140	22	US-10-868-337-1	Sequence 1, Appl
C 543	19	0.9	28118	21	US-10-600-009-403	Sequence 403, App	C 616	19	0.9	3673778	16	US-10-312-841-1	Sequence 1, Appl
C 544	19	0.9	29222	17	US-10-085-117-349	Sequence 349, App	C 617	19	0.9	3673778	16	US-10-312-841-2	Sequence 2, Appl
C 545	19	0.9	29993	21	US-10-482-823-3	Sequence 3, Appl	C 618	18	0.9	25	24	US-11-036-317-35082	Sequence 35082, A
C 546	19	0.9	29993	21	US-10-482-823-5	Sequence 5, Appl	C 619	18	0.9	25	24	US-11-036-317-613266	Sequence 613266, A
C 547	19	0.9	32591	17	US-10-085-117-187	Sequence 187, App	C 620	18	0.9	131	17	US-10-242-538A-44728	Sequence 44728, A
C 548	19	0.9	37154	19	US-10-741-601-5667	Sequence 5667, App	C 621	18	0.9	131	17	US-10-085-783A-44728	Sequence 44728, A
C 549	19	0.9	37154	20	US-10-719-993-6825	Sequence 6825, Ap	C 622	18	0.9	153	19	US-10-021-323-16395	Sequence 16395, A
C 550	19	0.9	38342	18	US-10-221-714B-472	Sequence 472, App	C 623	18	0.9	163	17	US-10-242-538A-8475	Sequence 8475, Ap
C 551	19	0.9	44851	20	US-10-719-993-6981	Sequence 6981, Ap	C 624	18	0.9	163	18	US-10-085-783A-8475	Sequence 8475, Ap
C 552	19	0.9	45121	11	US-09-997-722-10	Sequence 10, Appl	C 625	18	0.9	166	9	US-09-770-696-375	Sequence 375, App
C 553	19	0.9	48203	19	US-10-741-601-5711	Sequence 5711, Ap	C 626	18	0.9	174	9	US-09-770-696-325	Sequence 325, App
C 554	19	0.9	48203	21	US-10-741-600-17815	Sequence 17815, A	C 627	18	0.9	174	9	US-09-764-891-349	Sequence 349, App
C 555	19	0.9	55829	19	US-10-322-281-688	Sequence 688, App	C 628	18	0.9	174	9	US-09-764-891-349	Sequence 349, App
C 556	19	0.9	60500	13	US-10-087-192-1024	Sequence 1024, Ap	C 629	18	0.9	201	14	US-10-083-357-114	Sequence 114, App
C 557	19	0.9	65464	20	US-09-859-888-3	Sequence 3, Appl	C 630	18	0.9	201	14	US-10-719-993-42245	Sequence 42245, A
C 558	19	0.9	65464	20	US-10-476-543-3	Sequence 3, Appl	C 631	18	0.9	218	16	US-10-029-386-23914	Sequence 23914, A
C 559	19	0.9	71678	13	US-10-087-192-655	Sequence 655, App	C 632	18	0.9	230	17	US-10-242-538A-29917	Sequence 29917, A
C 560	19	0.9	73334	15	US-10-311-455-2097	Sequence 2097, Ap	C 633	18	0.9	230	17	US-10-085-783A-29917	Sequence 29917, A
C 561	19	0.9	73334	18	US-10-240-5890-127	Sequence 127, App	C 634	18	0.9	231	9	US-09-884-441-468	Sequence 468, App
C 562	19	0.9	76600	22	US-10-722-939-1	Sequence 1, Appl	C 635	18	0.9	231	10	US-09-907-969-468	Sequence 468, App
C 563	19	0.9	82938	10	US-09-818-657-3	Sequence 3, Appl	C 636	18	0.9	231	15	US-10-198-053-468	Sequence 468, App
C 564	19	0.9	82938	24	US-11-136-623-3	Sequence 3, Appl	C 637	18	0.9	234	21	US-10-860-790-468	Sequence 21717, A
C 565	19	0.9	83180	13	US-10-087-192-1405	Sequence 1405, Ap	C 638	18	0.9	242	19	US-10-437-963-21717	Sequence 20645, A
C 566	19	0.9	93011	20	US-10-719-993-6871	Sequence 6871, Ap	C 639	18	0.9	242	19	US-10-674-124A-20645	Sequence 20645, A
C 567	19	0.9	93483	17	US-10-034-650-49	Sequence 49, Appl	C 640	18	0.9	242	19	US-10-674-124A-25757	Sequence 25757, A
C 568	19	0.9	95835	13	US-10-087-192-1792	Sequence 1792, Ap	C 641	18	0.9	246	22	US-10-724-972A-1964	Sequence 1964, Ap
C 569	19	0.9	96595	18	US-10-052-482-232	Sequence 232, App	C 642	18	0.9	247	20	US-10-425-115-57396	Sequence 57396, A
C 570	19	0.9	96960	21	US-10-484-577-662	Sequence 662, App	C 643	18	0.9	259	19	US-10-437-963-35287	Sequence 35287, A
C 571	19	0.9	98844	21	US-10-467-182-10	Sequence 10, Appl	C 644	18	0.9	273	21	US-10-764-420-364	Sequence 364, App
C 572	19	0.9	102145	19	US-10-331-053-53	Sequence 53, Appl	C 645	18	0.9	273	21	US-10-424-599-108244	Sequence 108244, A
C 573	19	0.9	106236	21	US-10-741-600-17759	Sequence 17759, A	C 646	18	0.9	273	20	US-10-425-115-119746	Sequence 11447, A
C 574	19	0.9	107280	19	US-10-322-281-155	Sequence 155, App	C 647	18	0.9	281	20	US-10-425-115-108776	Sequence 108776, A
C 575	19	0.9	122923	13	US-10-087-192-268	Sequence 268, App	C 648	18	0.9	286	20	US-10-425-115-161368	Sequence 161368, A
C 576	19	0.9	129710	17	US-10-027-632-178902	Sequence 178902, A	C 649	18	0.9	287	11	US-09-732-627A-1828	Sequence 1828, Ap
C 577	19	0.9	129710	17	US-10-027-632-178902	Sequence 178902, A	C 650	18	0.9	287	11	US-10-424-599-108244	Sequence 108244, A
C 578	19	0.9	143412	13	US-10-087-192-997	Sequence 997, App	C 651	18	0.9	287	20	US-10-425-115-119746	Sequence 11447, A
C 579	19	0.9	152501	19	US-10-316-231-4	Sequence 4, Appl	C 652	18	0.9	294	19	US-10-674-124A-10883	Sequence 58208, A
C 580	19	0.9	162025	9	US-09-834-700-13	Sequence 13, Appl	C 653	18	0.9	295	19	US-10-424-599-58208	Sequence 41010, A
C 581	19	0.9	162025	9	US-09-834-700-14	Sequence 14, Appl	C 654	18	0.9	299	19	US-10-437-963-41010	Sequence 8, Appl
C 582	19	0.9	162025	9	US-09-834-700-17	Sequence 17, Appl	C 655	18	0.9	302	15	US-10-264-283-8	Sequence 46767, A
C 583	19	0.9	162025	9	US-09-834-700-18	Sequence 18, Appl	C 656	18	0.9	314	11	US-10-424-599-46767	Sequence 1063, Ap
C 584	19	0.9	162025	16	US-10-272-665-35	Sequence 35, Appl	C 657	18	0.9	316	11	US-09-864-408A-1063	Sequence 113506, A
C 585	19	0.9	162025	16	US-10-272-665-36	Sequence 36, Appl	C 658	18	0.9	326	18	US-10-424-599-113506	Sequence 115783, A
C 586	19	0.9	162025	16	US-10-273-321-35	Sequence 35, Appl	C 659	18	0.9	329	18	US-10-674-124A-9348	Sequence 9348, Ap
C 587	19	0.9	162025	16	US-10-273-321-36	Sequence 36, Appl	C 660	18	0.9	329	19	US-10-674-124A-9348	Sequence 4626, Ap
C 588	19	0.9	162025	16	US-10-272-756-35	Sequence 35, Appl	C 661	18	0.9	330	10	US-09-814-353-4626	Sequence 10925, A
C 589	19	0.9	162025	16	US-10-272-756-36	Sequence 36, Appl	C 662	18	0.9	330	10	US-09-814-353-4626	Sequence 10925, A
C 590	19	0.9	162025	17	US-10-273-228-35	Sequence 35, Appl	C 663	18	0.9	333	20	US-10-357-930-61672	Sequence 61672, A
C 591	19	0.9	162025	17	US-10-273-228-36	Sequence 36, Appl	C 664	18	0.9	336	22	US-10-724-972A-732	Sequence 732, App

665	18	0.9	337	18	US-10-424-599-13918	Sequence 13918, A	738	18	0.9	418	20	US-10-357-930-2244	Sequence 2244, Ap
666	18	0.9	337	20	US-10-425-115-113420	Sequence 113420, A	739	18	0.9	420	20	US-10-425-115-181784	Sequence 181784, Ap
667	18	0.9	339	20	US-10-357-930-12918	Sequence 12918, A	c 740	18	0.9	424	20	US-10-425-115-52807	Sequence 52807, A
c 668	18	0.9	339	22	US-10-724-972A-3176	Sequence 3176, Ap	741	18	0.9	425	18	US-10-424-599-115705	Sequence 115705, A
669	18	0.9	341	20	US-10-425-115-138884	Sequence 138884, A	c 742	18	0.9	426	10	US-09-814-353-18496	Sequence 18496, A
670	18	0.9	344	19	US-10-437-963-96105	Sequence 96105, A	c 743	18	0.9	428	13	US-10-027-632-273956	Sequence 273956, A
c 671	18	0.9	347	18	US-10-424-599-103550	Sequence 103550, A	c 744	18	0.9	428	17	US-10-027-632-273956	Sequence 273956, A
672	18	0.9	349	18	US-10-424-599-132938	Sequence 132938, A	c 745	18	0.9	428	20	US-10-357-930-14207	Sequence 14207, A
673	18	0.9	353	10	US-09-803-719-1218	Sequence 1218, Ap	c 746	18	0.9	429	12	US-09-925-065A-148388	Sequence 148388, A
674	18	0.9	353	22	US-10-779-543-14488	Sequence 14488, A	c 747	18	0.9	429	12	US-09-925-065A-148389	Sequence 148389, A
675	18	0.9	354	20	US-10-425-115-26048	Sequence 26048, A	c 748	18	0.9	429	12	US-09-925-065A-651275	Sequence 651275, A
676	18	0.9	355	18	US-10-424-599-84294	Sequence 84294, A	c 749	18	0.9	429	19	US-10-437-963-50818	Sequence 50818, A
677	18	0.9	357	18	US-10-424-599-62329	Sequence 62329, A	c 750	18	0.9	430	10	US-09-918-995-6348	Sequence 6348, Ap
678	18	0.9	359	15	US-10-046-955-23	Sequence 23, Appl	751	18	0.9	430	10	US-10-424-599-68040	Sequence 68040, A
679	18	0.9	360	12	US-09-925-065A-49040	Sequence 49040, A	c 752	18	0.9	431	20	US-10-425-115-127998	Sequence 127998, A
c 680	18	0.9	365	18	US-10-424-599-93941	Sequence 93941, A	753	18	0.9	432	20	US-09-770-423-114	Sequence 114, App
c 681	18	0.9	366	10	US-09-918-995-29907	Sequence 29907, A	754	18	0.9	434	9	US-09-728-445-694	Sequence 694, App
682	18	0.9	366	20	US-10-357-930-3749	Sequence 3749, Ap	c 755	18	0.9	434	9	US-09-960-352-3525	Sequence 3525, Ap
683	18	0.9	367	20	US-10-357-930-11413	Sequence 11413, A	c 755	18	0.9	434	22	US-10-964-549-694	Sequence 694, App
684	18	0.9	368	11	US-09-876-143-618	Sequence 618, App	756	18	0.9	435	10	US-09-814-353-13531	Sequence 13531, A
685	18	0.9	369	9	US-09-974-300-3818	Sequence 3818, Ap	757	18	0.9	435	12	US-09-925-065A-631751	Sequence 631751, A
c 686	18	0.9	375	18	US-10-424-599-128515	Sequence 128515, A	758	18	0.9	435	12	US-09-925-065A-631752	Sequence 631752, A
c 687	18	0.9	377	12	US-09-925-065A-134778	Sequence 134778, A	c 760	18	0.9	439	13	US-10-027-632-277919	Sequence 277919, A
c 688	18	0.9	377	20	US-10-425-115-1910	Sequence 1910, Ap	c 761	18	0.9	439	17	US-10-027-632-277919	Sequence 277919, A
c 689	18	0.9	379	18	US-10-424-599-102184	Sequence 102184, A	c 762	18	0.9	441	10	US-09-814-353-13628	Sequence 13628, A
c 690	18	0.9	382	19	US-10-674-144A-18472	Sequence 18472, A	763	18	0.9	444	10	US-09-814-353-1520	Sequence 1520, Ap
c 691	18	0.9	382	20	US-10-425-115-638	Sequence 638, App	764	18	0.9	444	10	US-09-814-353-7879	Sequence 7879, Ap
c 692	18	0.9	384	9	US-09-770-791-102	Sequence 102, App	c 765	18	0.9	445	9	US-09-983-965-3978	Sequence 3978, Ap
c 693	18	0.9	384	19	US-10-437-963-29145	Sequence 29145, A	766	18	0.9	445	12	US-09-925-065A-205717	Sequence 205717, A
694	18	0.9	384	20	US-10-425-115-118891	Sequence 118891, A	767	18	0.9	446	10	US-09-814-353-1503	Sequence 1503, Ap
c 695	18	0.9	385	10	US-09-814-353-878	Sequence 878, App	768	18	0.9	446	10	US-09-814-353-7862	Sequence 7862, Ap
c 696	18	0.9	385	10	US-09-814-353-7249	Sequence 7249, A	769	18	0.9	446	15	US-10-071-510-7	Sequence 7, Appl
c 697	18	0.9	389	18	US-10-424-599-24544	Sequence 24544, A	c 770	18	0.9	447	20	US-10-357-930-5038	Sequence 5038, Ap
c 698	18	0.9	389	20	US-10-425-115-14448	Sequence 14448, A	c 771	18	0.9	448	9	US-09-777-564-1170	Sequence 1170, Ap
c 699	18	0.9	390	9	US-09-777-564-977	Sequence 977, App	c 772	18	0.9	448	14	US-10-015-219-1170	Sequence 1170, Ap
c 700	18	0.9	390	9	US-09-777-564-1415	Sequence 1415, Ap	773	18	0.9	448	19	US-10-021-323-10901	Sequence 10901, A
c 701	18	0.9	390	14	US-10-015-219-977	Sequence 977, App	c 774	18	0.9	449	12	US-09-925-065A-522033	Sequence 522033, A
c 702	18	0.9	390	14	US-10-015-219-1415	Sequence 1415, Ap	c 775	18	0.9	452	17	US-10-242-535A-42236	Sequence 42236, A
c 703	18	0.9	390	18	US-10-424-599-14981	Sequence 14981, A	c 776	18	0.9	452	18	US-10-085-783A-42236	Sequence 42236, A
704	18	0.9	391	20	US-10-357-930-37444	Sequence 37444, A	c 777	18	0.9	456	20	US-10-357-930-9271	Sequence 9271, Ap
705	18	0.9	393	10	US-09-814-353-813	Sequence 813, App	c 778	18	0.9	462	10	US-09-918-995-13913	Sequence 13913, A
706	18	0.9	393	10	US-09-814-353-7185	Sequence 7185, Ap	779	18	0.9	462	10	US-09-814-353-894	Sequence 894, App
707	18	0.9	394	10	US-09-814-353-621	Sequence 621, App	780	18	0.9	462	10	US-09-814-353-7265	Sequence 7265, Ap
708	18	0.9	394	10	US-09-814-353-6998	Sequence 6998, Ap	781	18	0.9	463	10	US-09-814-353-1521	Sequence 1521, Ap
709	18	0.9	396	20	US-10-357-930-1325	Sequence 1325, App	782	18	0.9	463	10	US-09-814-353-7880	Sequence 7880, Ap
c 710	18	0.9	397	9	US-09-777-564-1148	Sequence 1148, Ap	783	18	0.9	463	12	US-09-925-065A-629368	Sequence 629368, A
c 711	18	0.9	397	14	US-10-015-219-1148	Sequence 1148, Ap	784	18	0.9	463	15	US-10-071-510-10	Sequence 10, Appl
c 712	18	0.9	398	9	US-09-777-564-1345	Sequence 1345, Ap	785	18	0.9	463	20	US-10-357-930-30474	Sequence 30474, A
c 713	18	0.9	398	14	US-10-015-219-1345	Sequence 1345, Ap	786	18	0.9	464	9	US-09-864-761-5329	Sequence 5329, Ap
c 714	18	0.9	399	18	US-10-424-599-8305	Sequence 8305, Ap	787	18	0.9	464	20	US-10-425-115-41771	Sequence 41771, A
715	18	0.9	399	18	US-10-424-599-29877	Sequence 29877, A	c 788	18	0.9	465	9	US-09-777-564-1023	Sequence 1023, Ap
716	18	0.9	400	20	US-10-425-115-177601	Sequence 177601, A	c 789	18	0.9	465	9	US-09-777-564-1462	Sequence 1462, Ap
717	18	0.9	400	20	US-10-357-930-47311	Sequence 47311, A	c 790	18	0.9	465	14	US-10-015-219-1023	Sequence 1023, Ap
c 718	18	0.9	400	12	US-09-925-065A-783137	Sequence 783137, A	c 791	18	0.9	465	14	US-10-015-219-1462	Sequence 1462, Ap
c 719	18	0.9	401	12	US-09-925-065A-783138	Sequence 783138, A	c 792	18	0.9	466	10	US-09-814-353-1449	Sequence 1449, Ap
c 720	18	0.9	402	9	US-09-880-107-1364	Sequence 1364, Ap	793	18	0.9	466	10	US-09-814-353-7810	Sequence 7810, Ap
c 721	18	0.9	404	10	US-09-918-995-8805	Sequence 8805, Ap	794	18	0.9	466	10	US-09-814-353-1419	Sequence 1419, Ap
c 722	18	0.9	406	12	US-09-925-065A-651276	Sequence 651276, A	c 795	18	0.9	467	10	US-09-814-353-7781	Sequence 7781, Ap
c 723	18	0.9	406	20	US-10-425-115-164311	Sequence 164311, A	c 796	18	0.9	468	20	US-10-357-930-56219	Sequence 56219, A
724	18	0.9	407	9	US-09-770-423-660	Sequence 660, App	c 797	18	0.9	469	10	US-09-814-353-13634	Sequence 13634, A
c 725	18	0.9	408	10	US-09-918-995-3718	Sequence 3718, Ap	798	18	0.9	469	18	US-10-424-599-22509	Sequence 22509, A
726	18	0.9	408	19	US-10-021-323-11090	Sequence 11090, A	799	18	0.9	470	9	US-09-783-590-12453	Sequence 12453, A
727	18	0.9	408	20	US-10-425-115-123610	Sequence 123610, A	800	18	0.9	470	10	US-09-814-353-617	Sequence 617, App
728	18	0.9	409	10	US-09-918-995-3982	Sequence 3982, Ap	801	18	0.9	470	10	US-09-814-353-6994	Sequence 6994, Ap
c 729	18	0.9	409	10	US-09-814-353-17309	Sequence 17309, A	802	18	0.9	470	20	US-10-357-930-32585	Sequence 32585, A
730	18	0.9	410	12	US-09-925-065A-638112	Sequence 638112, A	803	18	0.9	470	20	US-10-357-930-34070	Sequence 34070, A
731	18	0.9	410	12	US-09-925-065A-638113	Sequence 638113, A	804	18	0.9	470	20	US-10-357-930-41511	Sequence 41511, A
732	18	0.9	410	18	US-10-424-599-61494	Sequence 61494, A	805	18	0.9	470	20	US-10-357-930-42938	Sequence 42938, A
c 733	18	0.9	410	20	US-10-357-930-56415	Sequence 56415, A	c 806	18	0.9	472	12	US-09-925-065A-450855	Sequence 450855, A
734	18	0.9	415	10	US-09-814-353-2907	Sequence 2907, Ap	c 807	18	0.9	473	18	US-10-424-599-34978	Sequence 34978, A
735	18	0.9	415	10	US-09-814-353-9236	Sequence 9236, Ap	808	18	0.9	475	12	US-09-925-065A-165096	Sequence 165096, A
c 736	18	0.9	415	18	US-10-424-599-112318	Sequence 112318, A	809	18	0.9	476	22	US-10-972-079-858	Sequence 858, App
737	18	0.9	416	15	US-10-007-926A-284	Sequence 284, App	810	18	0.9	477	10	US-09-814-353-14255	Sequence 14255, A

811	18	0.9	477	13	US-10-027-632-65273	Sequence 65273, A	C 884	18	0.9	510	20	US-10-363-345A-16650	Sequence 16650, A
812	18	0.9	477	13	US-10-027-632-65274	Sequence 65274, A	C 885	18	0.9	510	21	US-10-363-483A-16649	Sequence 16649, A
813	18	0.9	477	17	US-10-027-632-65273	Sequence 65273, A	C 886	18	0.9	510	21	US-10-363-483A-16650	Sequence 16650, A
814	18	0.9	477	17	US-10-027-632-65274	Sequence 65274, A	C 887	18	0.9	511	12	US-09-814-353-14274	Sequence 14274, A
815	18	0.9	477	17	US-10-027-632-65274	Sequence 65274, A	C 888	18	0.9	511	12	US-09-814-353-14274	Sequence 14274, A
816	18	0.9	477	17	US-10-085-783A-29901	Sequence 29901, A	C 889	18	0.9	511	12	US-09-925-065A-755667	Sequence 755667, A
817	18	0.9	477	17	US-10-085-783A-29901	Sequence 29901, A	C 889	18	0.9	512	12	US-09-925-065A-755667	Sequence 755667, A
818	18	0.9	477	20	US-10-425-115-137159	Sequence 137159, A	C 890	18	0.9	512	12	US-09-925-065A-755667	Sequence 755667, A
819	18	0.9	477	20	US-09-918-995-35423	Sequence 35423, A	C 891	18	0.9	512	12	US-09-925-065A-755667	Sequence 755667, A
820	18	0.9	478	13	US-10-027-632-184293	Sequence 184293, A	C 892	18	0.9	512	18	US-10-424-599-314	Sequence 314, App
821	18	0.9	478	17	US-10-027-632-184293	Sequence 184293, A	C 893	18	0.9	513	18	US-10-424-599-314	Sequence 314, App
822	18	0.9	479	18	US-10-424-599-113649	Sequence 113649, A	C 894	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
823	18	0.9	479	20	US-10-357-930-35328	Sequence 35328, A	C 895	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
824	18	0.9	479	20	US-10-357-930-35328	Sequence 35328, A	C 896	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
825	18	0.9	480	9	US-09-777-564-929	Sequence 929, App	C 897	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
826	18	0.9	480	10	US-09-814-353-13768	Sequence 13768, A	C 898	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
827	18	0.9	480	12	US-09-925-065A-474626	Sequence 474626, A	C 899	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
828	18	0.9	480	12	US-09-925-065A-474627	Sequence 474627, A	C 900	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
829	18	0.9	480	14	US-10-015-219-929	Sequence 929, App	C 901	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
830	18	0.9	481	10	US-09-814-353-4944	Sequence 4944, App	C 902	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
831	18	0.9	481	13	US-10-027-633-193998	Sequence 193998, A	C 903	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
832	18	0.9	481	17	US-10-027-633-193998	Sequence 193998, A	C 904	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
833	18	0.9	482	12	US-09-925-065A-130199	Sequence 130199, A	C 905	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
834	18	0.9	482	20	US-10-357-930-49174	Sequence 49174, A	C 906	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
835	18	0.9	484	20	US-10-723-860-1395	Sequence 1395, App	C 907	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
836	18	0.9	485	9	US-09-833-790-58	Sequence 58, App1	C 908	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
837	18	0.9	485	12	US-09-925-065A-350643	Sequence 350643, A	C 909	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
838	18	0.9	485	12	US-09-925-065A-350644	Sequence 350644, A	C 910	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
839	18	0.9	485	12	US-09-925-065A-350645	Sequence 350645, A	C 911	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
840	18	0.9	485	12	US-09-925-065A-350646	Sequence 350646, A	C 912	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
841	18	0.9	486	10	US-09-814-353-13650	Sequence 13650, A	C 913	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
842	18	0.9	488	10	US-09-814-353-1447	Sequence 1447, App	C 914	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
843	18	0.9	488	10	US-09-814-353-1531	Sequence 1531, App	C 915	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
844	18	0.9	488	10	US-09-814-353-7808	Sequence 7808, App	C 916	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
845	18	0.9	488	10	US-09-814-353-7890	Sequence 7890, App	C 917	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
846	18	0.9	488	10	US-09-814-353-7890	Sequence 7890, App	C 918	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
847	18	0.9	488	22	US-10-071-510-9	Sequence 9, App1	C 919	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
848	18	0.9	490	20	US-10-972-079-79086	Sequence 79086, A	C 920	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
849	18	0.9	490	22	US-10-972-079-857	Sequence 857, App	C 921	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
850	18	0.9	491	12	US-09-925-065A-383591	Sequence 383591, A	C 922	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
851	18	0.9	491	12	US-09-925-065A-938715	Sequence 938715, A	C 923	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
852	18	0.9	491	20	US-10-723-860-2873	Sequence 2873, App	C 924	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
853	18	0.9	492	10	US-09-814-353-14246	Sequence 14246, A	C 925	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
854	18	0.9	497	10	US-09-814-353-1456	Sequence 1456, App	C 926	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
855	18	0.9	497	10	US-09-814-353-1456	Sequence 1456, App	C 927	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
856	18	0.9	497	15	US-09-814-353-7817	Sequence 7817, App	C 928	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
857	18	0.9	497	15	US-10-071-510-8	Sequence 8, App1	C 929	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
858	18	0.9	497	19	US-10-437-963-85578	Sequence 85578, A	C 930	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
859	18	0.9	498	10	US-09-814-353-1512	Sequence 1512, App	C 931	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
860	18	0.9	498	10	US-09-814-353-7871	Sequence 7871, App	C 932	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
861	18	0.9	498	12	US-09-925-065A-566432	Sequence 566432, A	C 933	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
862	18	0.9	500	20	US-10-425-115-68926	Sequence 68926, A	C 934	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
863	18	0.9	502	17	US-10-242-535A-13950	Sequence 13950, A	C 935	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
864	18	0.9	502	17	US-10-085-783A-13950	Sequence 13950, A	C 936	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
865	18	0.9	502	20	US-10-425-115-57498	Sequence 57498, A	C 937	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
866	18	0.9	503	10	US-09-814-353-14202	Sequence 14202, A	C 938	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
867	18	0.9	503	10	US-09-814-353-14263	Sequence 14263, A	C 939	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
868	18	0.9	503	10	US-09-814-353-14263	Sequence 14263, A	C 940	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
869	18	0.9	503	12	US-09-925-065A-805846	Sequence 805846, A	C 941	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
870	18	0.9	503	20	US-10-357-930-60821	Sequence 60821, A	C 942	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
871	18	0.9	504	10	US-09-814-353-13570	Sequence 13570, A	C 943	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
872	18	0.9	504	18	US-10-424-599-141347	Sequence 141347, A	C 944	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
873	18	0.9	505	12	US-09-925-065A-420355	Sequence 420355, A	C 945	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
874	18	0.9	505	12	US-09-925-065A-580184	Sequence 580184, A	C 946	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
875	18	0.9	505	12	US-09-925-065A-580185	Sequence 580185, A	C 947	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
876	18	0.9	505	12	US-09-925-065A-580186	Sequence 580186, A	C 948	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
877	18	0.9	505	20	US-10-363-345A-2065	Sequence 2065, App	C 949	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
878	18	0.9	505	20	US-10-363-345A-2066	Sequence 2066, App	C 950	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
879	18	0.9	505	21	US-10-363-483A-2066	Sequence 2066, App	C 951	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
880	18	0.9	505	21	US-10-363-483A-2066	Sequence 2066, App	C 952	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
881	18	0.9	509	12	US-09-925-065A-556031	Sequence 556031, A	C 953	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
882	18	0.9	510	19	US-10-021-323-677	Sequence 677, App	C 954	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A
883	18	0.9	510	20	US-10-363-345A-16649	Sequence 16649, A	C 955	18	0.9	513	18	US-09-814-353-15748	Sequence 15748, A

Db	1021	GTCTAACCGAACAACGATCGTTATGAGCCCAACGAGCAAGAGGGTAAACCGAGAA	1080
Qy	1081	AGAGGGGATCGCAAAATCGTAATAAACAAGGAAATAAAGGGTGGTTTCCACGATAGTC	1140
Db	1081	AGAGGGGATCGCAAAATCGTAATAAACAAGGAAATAAAGGGTGGTTTCCACGATAGTC	1140
Qy	1141	TGCTATATGACGCGAAGGGTTCTTAATTCAGAGAGCAATTAATCAGTTTCGTGTG	1200
Db	1141	TGCTATATGACGCGAAGGGTTCTTAATTCAGAGAGCAATTAATCAGTTTCGTGTG	1200
Qy	1201	TTTGGAGAAAGAAGAACAGATCAATACGAGAGAGATCTCTAAAGAGATTATCGTT	1260
Db	1201	TTTGGAGAAAGAAGAACAGATCAATACGAGAGAGATCTCTAAAGAGATTATCGTT	1260
Qy	1261	TCAAGTAAGTCTCTTTATCAAACTCTTAATAATAAACAATCAAAACAATGAACACGTCGTG	1320
Db	1261	TCAAGTAAGTCTCTTTATCAAACTCTTAATAATAAACAATCAAAACAATGAACACGTCGTG	1320
Qy	1321	TCCTCGTTTCGATCTAGATACGATTTTTCGAGAAATTACGAGAGAACTCTGTTTATTAC	1380
Db	1321	TCCTCGTTTCGATCTAGATACGATTTTTCGAGAAATTACGAGAGAACTCTGTTTATTAC	1380
Qy	1381	TACTAGGTTGTTCAATATTTTCCGAGAAATTACGAGAGAACTCTGTTTATTAC	1440
Db	1381	TACTAGGTTGTTCAATATTTTCCGAGAAATTACGAGAGAACTCTGTTTATTAC	1440
Qy	1441	TGATGACAGATGATGAAGTAATATATATACATAAATCATGTTTGTCTCAAGCATCTACGT	1500
Db	1441	TGATGACAGATGATGAAGTAATATATATACATAAATCATGTTTGTCTCAAGCATCTACGT	1500
Qy	1501	TGAATATATATAAGAAATTTTTCGAGAAATAATGATGAGAAATTCATCTTTC	1560
Db	1501	TGAATATATATAAGAAATTTTTCGAGAAATAATGATGAGAAATTCATCTTTC	1560
Qy	1561	ATAATAGTGAACAACTCTCTTTCATACCAAAAAAATTTGAAAAAATAGTGA	1620
Db	1561	ATAATAGTGAACAACTCTCTTTCATACCAAAAAAATTTGAAAAAATAGTGA	1620
Qy	1621	CTCTCTTTGTCGATAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATAACA	1680
Db	1621	CTCTCTTTGTCGATAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATAACA	1680
Qy	1681	ATTTTTCGATGCAATATGTTCTGAGTAAATATACCAATAGAAACATATTTTA	1740
Db	1681	ATTTTTCGATGCAATATGTTCTGAGTAAATATACCAATAGAAACATATTTTA	1740
Qy	1741	GGAGTAGTAAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAAATTTCTTTTG	1800
Db	1741	GGAGTAGTAAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAAATTTCTTTTG	1800
Qy	1801	CTGTTCTTTGTTTGTGTTTTATAGAACATTCGAATATGATGATTTTTCCTTTCACC	1860
Db	1801	CTGTTCTTTGTTTGTGTTTTATAGAACATTCGAATATGATGATTTTTCCTTTCACC	1860
Qy	1861	AGTAGATATGATATACACATATAGTAACATCGGTAGTTTATATAGAGAGAGATTGA	1920
Db	1861	AGTAGATATGATATACACATATAGTAACATCGGTAGTTTATATAGAGAGAGATTGA	1920
Qy	1921	TTTTTCGATATTTCTTTTGTGAAAAATAATATGTTGAAAAATTTATTTTATTAATTT	1980
Db	1921	TTTTTCGATATTTCTTTTGTGAAAAATAATATGTTGAAAAATTTATTTTATTAATTT	1980
Qy	1981	GACAGATTGTTTCAGTTGAGAAGTTTAAATTTAGATTAAACACAAAAAG	2030
Db	1981	GACAGATTGTTTCAGTTGAGAAGTTTAAATTTAGATTAAACACAAAAAG	2030

RESULT 2
US-10-643-676-2
; Sequence 2, Application US/10643676
; Publication No. US20050176946A1
; GENERAL INFORMATION:

; APPLICANT: Thomas, Terry
; APPLICANT: Nuccio, Michael
; APPLICANT: Heieh, Tzung-Fu
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis
; FILE REFERENCE: A35897-PC1-USA-A (072667.0188)
; CURRENT APPLICATION NUMBER: US/10/643,676
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: PCT/EP02/02894
; PRIOR FILING DATE: February 14, 2002
; PRIOR APPLICATION NUMBER: 60/270,779
; PRIOR FILING DATE: February 22, 2001
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2042
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-643-676-2

Query Match	100.0%;	Score 2030;	DB 22;	Length 2042;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2030;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTTCATAGAGGATGGACCAATTAAGAAATACCTTTCTCTTTCTATTTTATTTGATTAG	60	
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Qy	61	AAATCATATTCATTCAAAAGGAAAAAATAATTTTCTATCTCTAAAGTTATAAC	120	
Db	67	AAATCATATTCATTCAAAAGGAAAAAATAATTTTCTATCTCTAAAGTTATAAC	126	
Qy	121	TTACAAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTG	180	
Db	127	TTACAAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTG	186	
Qy	181	TTTTAGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAATGNAAT	240	
Db	187	TTTTAGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAATGNAAT	246	
Qy	241	GGGTTTCAACTATTTTATCGTTTGACACTTACACTTATCAAAAGAGTTCAAAATA	300	
Db	247	GGGTTTCAACTATTTTATCGTTTGACACTTACACTTATCAAAAGAGTTCAAAATA	306	
Qy	301	AAAAATAGAAATCGAATCAACCGTTTCAGTGTAAAGGGATTTGATATCGTCAATTT	360	
Db	307	AAAAATAGAAATCGAATCAACCGTTTCAGTGTAAAGGGATTTGATATCGTCAATTT	366	
Qy	361	TAAAGAGTTGTTTGTGTTTTTTTCCAACTCTGCAATGTTTTCGTTCCGTTGAACCAAT	420	
Db	367	TAAAGAGTTGTTTGTGTTTTTTTCCAACTCTGCAATGTTTTCGTTCCGTTGAACCAAT	426	
Qy	421	TCAACACTTTGTATTAACCGAATAGTAATATCTAGACGTACGCAATACCAAAATAA	480	
Db	427	TCAACACTTTGTATTAACCGAATAGTAATATCTAGACGTACGCAATACCAAAATAA	486	
Qy	481	ATTAAAACTCAATTCACAAATTCGAATCTACACCATATCATGCATATATATCAGCAACTA	540	
Db	487	ATTAAAACTCAATTCACAAATTCGAATCTACACCATATCATGCATATATATCAGCAACTA	546	
Qy	541	GAATAATCAATGAAATTTAATTCAGGAGTAATCAATATCCAACTCAACGATTAATCAAAAGC	600	
Db	547	GAATAATCAATGAAATTTAATTCAGGAGTAATCAATATCCAACTCAACGATTAATCAAAAGC	606	
Qy	601	CTAATAATAGATCAATGAAATCAATTAACATAGTAATATACATGATTGTTGTTA	660	
Db	607	CTAATAATAGATCAATGAAATCAATTAACATAGTAATATACATGATTGTTGTTA	666	
Qy	661	AACAGAAATAATACATTAATAGTATGAAATATGAATATATATATAGATAAGAGGCGTA	720	
Db	667	AACAGAAATAATACATTAATAGTATGAAATATGAATATATATATAGATAAGAGGCGTA	726	
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Db 727 TATGTTACAACTACAGATCACCATCCACAATTAACAATCGATTGGTGGGCCATTGTT 786
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Db 787 TCGATATTTGCCAACTGTGATGATGACTGCCAGCTGGCATATATTTTCCCCTCTCGATT 846
Qy 841 AGTGTATTTACCTTTCCCTCTCTGTTTACCGTTAAATTCAAATTTTACTATTTGTACCGCT 900
Db 847 AGTGTATTTACCTTTCCCTCTCTGTTTACCGTTAAATTCAAATTTTACTATTTGTACCGCT 906
Qy 901 GTCTTTTCACTTTTAAAGAAACCCCAACCCGAAATCATAACTATACCCGAAATCACATGT 960
Db 907 GTCTTTTCACTTTTAAAGAAACCCCAACCCGAAATCATAACTATACCCGAAATCACATGT 966
Qy 961 CTTTCATGGTGAAGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAAACCTATTTGAGATT 1020
Db 967 CTTTCATGGTGAAGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAAACCTATTTGAGATT 1026
Qy 1021 GTGCTAACCGAAACAGAACCGTTATGACGCCAACCGGCAAGAGGGGTAAACCGAGAA 1080
Db 1027 GTGCTAACCGAAACAGAACCGTTATGACGCCAACCGGCAAGAGGGGTAAACCGAGAA 1086
Qy 1081 AGAGGGGATGGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGGTTTCAAGATAAGTC 1140
Db 1087 AGAGGGGATGGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGGTTTCAAGATAAGTC 1146
Qy 1141 TGTCTATATGACCGGAAAGGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTTCGTGTG 1200
Db 1147 TGTCTATATGACCGGAAAGGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTTCGTGTG 1206
Qy 1201 TTTGGAGAGAGAAAGAACAGATCAATACGAGGAGAGATCTCTAAGAGATTTATCGTT 1260
Db 1207 TTTGGAGAGAGAAAGAACAGATCAATACGAGGAGAGATCTCTAAGAGATTTATCGTT 1266
Qy 1261 TCAAGTAAGTCTCTTTATCAAACTCTTATATATAAACAATCAAAACATGAACACGTCGTG 1320
Db 1267 TCAAGTAAGTCTCTTTATCAAACTCTTATATATAAACAATCAAAACATGAACACGTCGTG 1326
Qy 1321 TCTTCGTTTCGATTCAGATACAGATTTTTCAGAGATTTAGTTTCATGTGAATGAACCTCTGTTTAAATAC 1380
Db 1327 TCTTCGTTTCGATTCAGATACAGATTTTTCAGAGATTTAGTTTCATGTGAATGAACCTCTGTTTAAATAC 1386
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Db 1387 TACTACGGTGTGTCATATATTTTCCAGAGATTTACAGAGAGAACAAAGTTAGTGATATAT 1446
Qy 1441 TGATGCAGAGTATGAAGTAAATATATACATAAATCATGTTTGTCTCAAGCATCTACGT 1500
Db 1447 TGATGCAGAGTATGAAGTAAATATATACATAAATCATGTTTGTCTCAAGCATCTACGT 1506
Qy 1501 TGAATATATATAAGAAAGTTTTTTTTTGGTGAAAAAATATGATGAGAAAGTTTCATCTTTC 1560
Db 1507 TGAATATATATAAGAAAGTTTTTTTTTGGTGAAAAAATATGATGAGAAAGTTTCATCTTTC 1566
Qy 1561 ATAATAGTGAACAACTCTCTTTTCATACCAAAAAAATTTTCAAAAAAATTTAGTGAAA 1620
Db 1567 ATAATAGTGAACAACTCTCTTTTCATACCAAAAAAATTTTCAAAAAAATTTAGTGAAA 1626
Qy 1621 CTCCTCTTGTCCGATTTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTTAGCATACAA 1680
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Qy 1681 ATTTTGTGGATGGCAATTTATGTCGTCAGGTAATAATATACCAATAGAAACATATTTTAA 1740
Db 1687 ATTTTGTGGATGGCAATTTATGTCGTCAGGTAATAATATACCAATAGAAACATATTTTAA 1746
Qy 1741 GGAAGTATTAAGATTTATGTTGAAGAAATACTATACGATAAGCAATAAATTTCTTTTG 1800
Db 1747 GGAAGTATTAAGATTTATGTTGAAGAAATACTATACGATAAGCAATAAATTTCTTTTG 1806
Qy 1801 CTGTTCTTGTGTTTTTGTGTTTTTATAGAAACATTTGAATATGACTTTTGTGTTTTTTCACC 1860
Db 1807 CTGTTCTTGTGTTTTTGTGTTTTTATAGAAACATTTGAATATGACTTTTGTGTTTTTTCACC 1866

RESULT 3

US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152

Query Match 52.4%; Score 1064; DB 9; Length 1064;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 GGTGACGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAACTTATGAGATTGTGCTA 1026
Db 1 GGTGACGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAACTTATGAGATTGTGCTA 60
Qy 1027 ACCGAAAAACAGAAACCGTTATGACGCCAACGAGGCAAGAGGGGTAAACCGAGAAAGAGG 1086
Db 61 ACCGAAAAACAGAAACCGTTATGACGCCAACGAGGCAAGAGGGGTAAACCGAGAAAGAGG 120
Qy 1087 GATGCGAGAAATCGTAAATTAACAAGAAAAATAAAGGGTGGTTTTCAGATAAGTCTGTCTA 1146
Db 121 GATGCGAGAAATCGTAAATTAACAAGAAAAATAAAGGGTGGTTTTCAGATAAGTCTGTCTA 180
Qy 1147 TATGACGCGAAAGGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTGGA 1206
Db 181 TATGACGCGAAAGGGTTCTTAAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTGGA 240
Qy 1207 GAAGAGAGAGACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGT 1266
Db 241 GAAGAGAGAGACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGT 300
Qy 1267 AAGTCTCTTTTATCAAACTCTTAAATTAACAACAAATCAAAACATGAACACGTCGTCTTCG 1326
Db 301 AAGTCTCTTTTATCAAACTCTTAAATTAACAACAAATCAAAACATGAACACGTCGTCTTCG 360
Qy 1327 TTTTCGATTCAGATACGATTTTTCAGTGAATGAACTCTCTTTTATTTACTACTAG 1386
Db 361 TTTTCGATTCAGATACGATTTTTCAGTGAATGAACTCTCTTTTATTTACTACTAG 420

1387 GGTGTTGTCATATATTTTCCGAGAAATTACACAGAGAAACAAAGTTAGTGATTATATATGATGC 1446
1447 AGAGTATGAAGTAAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 1506
481 AGAGTATGAAGTAAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 540
1507 ATATATAAGAAAGTTTGTGTAAGAAATATGATGAGAAATTCATCTTTTCATAAATA 1566
541 ATATATAAGAAAGTTTGTGTAAGAAATATGATGAGAAATTCATCTTTTCATAAATA 600
1567 GTCAAAACAACTCTCTTTTCATACCAAAACAAATTTGAAACAAATTTAGTGAACCTCTCT 1626
601 GTCAAAACAACTCTCTTTTCATACCAAAACAAATTTGAAACAAATTTAGTGAACCTCTCT 660
1627 TTGTCGCGATTAGTTAGTTAGTTGGAATCAGAAATCAAAATACGATTAGCATAAACAAATTTT 1686
661 TTGTCGCGATTAGTTAGTTAGTTGGAATCAGAAATCAAAATACGATTAGCATAAACAAATTTT 720
1687 TGGCATGGCAATTAATGTCGTCAGGTAAATATACCAATAGAAACATATTTTGGAGTA 1746
721 TGGCATGGCAATTAATGTCGTCAGGTAAATATACCAATAGAAACATATTTTGGAGTA 780
1747 GTTAAGATTAATGTTGAAGAAATACCTATACGATAGCAATTAATTTCTTTGCTGTTTC 1806
781 GTTAAGATTAATGTTGAAGAAATACCTATACGATAGCAATTAATTTCTTTGCTGTTTC 840
1807 TTGTTTTGCTGTTTTATAGAACATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
841 TTGTTTTGCTGTTTTATAGAACATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 900
1867 TATGTTACTATACACATAAGTAACTAGTGGTAGTTTATATAGAGAGAGATTTGATTTTTC 1926
901 TATGTTACTATACACATAAGTAACTAGTGGTAGTTTATATAGAGAGAGATTTGATTTTTC 960
1927 GTATATTTCTTTGTCGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
961 GTATATTTCTTTGTCGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
1987 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTTAAACAAACAAAAG 2030
1021 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTTAAACAAACAAAAG 1064

RESULT 4
US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938.842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152

Query Match 52.4%; Score 1064; DB 11; Length 1064;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 967 GGTGCGTAAACAGAACTTATTTTCCGGTTGAATTTGTTTAACTATTGAGATTGTGCTA 1026
DB 1 GGTGCGTAAACAGAACTTATTTTCCGGTTGAATTTGTTTAACTATTGAGATTGTGCTA 60
QY 1027 ACCGAAAAACAGAAACGGTTTATGACGCCAACGAGGCGAAGGGGTAAAAACGAGAAAGGG 1086
DB 61 ACCGAAAAACAGAAACGGTTTATGACGCCAACGAGGCGAAGGGGTAAAAACGAGAAAGGG 120
QY 1087 GATGCGAGAAATCGTAAATTAACAGGAAATTAAGGGTGGTTTTCAGATAAGTCTGCTA 1146
DB 121 GATGCGAGAAATCGTAAATTAACAGGAAATTAAGGGTGGTTTTCAGATAAGTCTGCTA 180
QY 1147 TATGCGCGAAAGGGTCTTCTTAAATTCAGAGAGACAATTAATCAGTTTCTGTTGTTTGA 1206
DB 181 TATGCGCGAAAGGGTCTTCTTAAATTCAGAGAGACAATTAATCAGTTTCTGTTGTTTGA 240
QY 1207 GAAGAAAGAAACAGATCAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGT 1266
DB 241 GAAGAAAGAAACAGATCAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGT 300
QY 1267 AGTCTCTTTTATCAAACTCTTAAATTAACAAATCAAAACATCAACACGTCGTCTTCG 1326
DB 301 AGTCTCTTTTATCAAACTCTTAAATTAACAAATCAAAACATCAACACGTCGTCTTCG 360
QY 1327 TTTTCGATCTAGATACGATTTTTCATGTAAGTAACTCTGTTTATTAATACTACTAG 1386
DB 361 TTTTCGATCTAGATACGATTTTTCATGTAAGTAACTCTGTTTATTAATACTACTAG 420
QY 1387 GGTGTTGTCATATTTTTCGAGAAATTTACAGAGAGAAACAAAGTTAGTGATTTATGATGC 1446
DB 421 GGTGTTGTCATATTTTTCGAGAAATTTACAGAGAGAAACAAAGTTAGTGATTTATGATGC 480
QY 1447 AGAGTATGAAGTAAATTAATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 1506
DB 481 AGAGTATGAAGTAAATTAATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 540
QY 1507 ATATATAAGAAAGTTTGTGTAAGAAATATGATGAGAAATTTGAAACAAATTTTTCATAATA 1566
DB 541 ATATATAAGAAAGTTTGTGTAAGAAATATGATGAGAAATTTGAAACAAATTTTTCATAATA 600
QY 1567 GTCAAAACAACTCTCTTTTCATACCAAAACAAATTTGAAACAAATTTAGTGAACCTCTCT 1626
DB 601 GTCAAAACAACTCTCTTTTCATACCAAAACAAATTTGAAACAAATTTAGTGAACCTCTCT 660
QY 1627 TTGTCGCGATTAGTTAGTTAGTTGGAATCAGAAATCAAAATACGATTAGCATAAACAAATTTT 1686
DB 661 TTGTCGCGATTAGTTAGTTAGTTGGAATCAGAAATCAAAATACGATTAGCATAAACAAATTTT 720
QY 1687 TGGCATGGCAATTAATGTCGTCAGGTAAATATACCAATAGAAACATATTTTGGAGTA 1746
DB 721 TGGCATGGCAATTAATGTCGTCAGGTAAATATACCAATAGAAACATATTTTGGAGTA 780
QY 1747 GTTAAGATTAATGTTGAAGAAATACCTATACGATAGCAATTAATTTCTTTGCTGTTTC 1806
DB 781 GTTAAGATTAATGTTGAAGAAATACCTATACGATAGCAATTAATTTCTTTGCTGTTTC 840
QY 1807 TTGTTTTGCTGTTTTATAGAACATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
DB 841 TTGTTTTGCTGTTTTATAGAACATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1867 TATGTTACTATACACATAAGTAACTAGTGGTAGTTTATATAGAGAGAGATTTGATTTTTC 1926
DB 901 TATGTTACTATACACATAAGTAACTAGTGGTAGTTTATATAGAGAGAGATTTGATTTTTC 960
QY 1927 GTATATTTCTTTGTCGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
DB 961 GTATATTTCTTTGTCGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
1987 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTTAAACAAACAAAAG 2030

Db 1021 TTTGTTCCAGTCAGAGTTTAATTAGATTAAACAACAAG 1064

RESULT 5

US-09-770-445-116/c
; Sequence 116, Application US/09770445
; Patent No. US2002023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-116

Query Match 2.6%; Score 53; DB 9; Length 1088;
Best Local Similarity 100.0%; Pred. No. 28-11;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 AGAAGAACAGATCAAAATACGAGAGAGATCTCTAAAGAGATTTATCGTTTCAA 1264
Db 1066 AGAGAACAGATCAAAATACGAGAGAGATCTCTAAAGAGATTTATCGTTTCAA 1014

RESULT 6

US-10-424-599-140376/c
; Sequence 140376, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 140376
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97769C.1
US-10-424-599-140376

Query Match 1.2%; Score 25; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 AAAAGGAAAAAATAATATTTTT 102
Db 43 AAAAGGAAAAAATAATATTTTT 19

RESULT 7

US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 1.2%; Score 25; DB 16; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1503 AAATATATATAAGAAAGTTTTTTTT 1527
Db 1630300 AAATATATATAAGAAAGTTTTTTTT 1630324

RESULT 8

US-09-925-065A-434756/c
; Sequence 434756, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 434756
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-434756

Query Match 1.2%; Score 24; DB 12; Length 558;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1592 AAAAAAAAAATTGAAAAAATTAG 1615
DB 313 AAAAAAAAAATTGAAAAAATTAG 290

RESULT 9
US-10-425-115-145853/c
; Sequence 145853, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 145853
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_64531C.1
US-10-425-115-145853

Query Match 1.1%; Score 23; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 AAGCAAAAAAAAAAATAATTTTT 102
DB 108 AAGCAAAAAAAAAAATAATTTTT 86

RESULT 10
US-10-108-260A-2360/c
; Sequence 2360, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2360

Query Match 1.1%; Score 23; DB 17; Length 2550;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1928 TATATTTCTTTTGTGAAATATA 1950
DB 1783 TATATTTCTTTTGTGAAATATA 1761

RESULT 11
US-10-425-115-101814/c
; Sequence 101814, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

QY 1592 AAAAAAAAAATTGAAAAAATTAG 1611
DB 149 AAAAAAAAAATTGAAAAAATTAG 128

RESULT 12
US-10-357-930-60834/c
; Sequence 60834, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60834
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-60834

Query Match 1.1%; Score 22; DB 20; Length 468;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAAAAATTGAAAAAATTAG 1611
DB 149 AAAAAAAAAATTGAAAAAATTAG 128

RESULT 13
US-09-925-065A-297974
; Sequence 297974, Application US/09925065A
; Publication No. US20050228172A9
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```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297974
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-297974
```

```
Query Match      1.1%; Score 22; DB 12; Length 574;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      73 ATTACAAAAGGAAAAAAAAT 94
Db      443 ATTACAAAAGGAAAAAAAAT 464
```

RESULT 14

```
US-09-925-065A-458650/c
; Sequence 458650, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458650
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-458650
```

```
Query Match      1.1%; Score 22; DB 12; Length 595;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1590 AAAAAAAAAATTGAAAAAAA 1611
Db      262 AAAAAAAAAATTGAAAAAAA 241
```

RESULT 15

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US-09-925-065A-458651/c
; Sequence 458651, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458651
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-458651
```

```
Query Match      1.1%; Score 22; DB 12; Length 595;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1590 AAAAAAAAAATTGAAAAAAA 1611
Db      262 AAAAAAAAAATTGAAAAAAA 241
```

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Job time : 2599 secs

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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 00:50:38 ; Search time 6676 Seconds

(without alignments)
11574.366 Million cell updates/sec

Title: US-10-643-676-1

Perfect score: 2030

Sequence: 1 cttcatagaagtgatggacca.....ttagatttaaacacaaaaag 2030

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- EST:.*
1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gest1:.*
9: gb_gest2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	426	21.0	426	9	CC796106 SALK_0928
C 2	395	18.5	679	8	AQ961292 LERFK31TF
C 3	368	18.1	679	8	AQ961293 LERFK31TR
4	258	12.7	412	8	B2597205 SALK_1004
C 5	118	5.8	982	9	CL489509 SAIL_525
6	112	5.5	194	9	CF402809 Arabidops
C 7	103	5.1	246	8	BH809771 SALK_0056
C 8	95	4.7	396	9	CC796100 SALK_0927
9	88	4.3	207	1	AV832342 AV832342
10	88	4.3	278	1	AJ609323 AJ609323
11	86	4.2	507	1	AV825689 AV825689
C 12	86	4.2	605	5	BP562932 BP562932
13	84	4.1	463	7	T43139 T43139
14	84	4.1	495	7	T43150 T43150
15	83	4.1	516	7	H36351 H36351
16	79	3.9	636	5	BP561393 BP561393
17	78	3.8	515	7	CK119189 CK119189
18	78	3.8	894	7	CF652281 CF652281
19	74	3.6	314	7	T88394 T88394
20	74	3.6	569	7	T41663 T41663
21	67	3.3	349	7	T13967 T13967
22	67	3.3	400	7	T04382 T04382
23	66	3.3	362	7	N38594 N38594
24	66	3.3	422	7	R64904 R64904

25	65	3.2	429	7	R64851	R64851	13355	Lambd
26	65	3.2	487	7	H77166	H77166	17597	Lambd
27	65	3.2	554	7	H37321	H37321	15450	Lambd
28	63	3.1	438	7	T76560	T76560	11338	Lambd
29	61	3.0	391	7	T45222	T45222	7785	Lambd
30	61	3.0	484	7	T45972	T45972	9235	Lambd
31	61	3.0	545	7	H36812	H36812	14941	Lambd
32	60	3.0	484	7	CK119252	CK119252	213101.p1	
33	59	2.9	380	7	R64820	R64820	13324	Lambd
34	59	2.9	381	7	R65167	R65167	13671	Lambd
35	59	2.9	425	7	N65161	N65161	20201	Lambd
36	59	2.9	428	7	T75683	T75683	10461	Lambd
37	59	2.9	441	7	T43969	T43969	7232	Lambd
38	58	2.9	379	7	T44460	T44460	7723	Lambd
39	58	2.9	441	7	T76049	T76049	10827	Lambd
40	58	2.9	525	7	N38557	N38557	19784	Lambd
41	57	2.8	394	7	T22253	T22253	4261	Lambd
42	57	2.8	748	7	CK117722	CK117722	214h23.p1	
43	56	2.8	1318	3	CNS0A2U5	CNS0A2U5	7666	Arabidops
44	55	2.7	442	7	N96915	N96915	22290	Lambd
45	55	2.7	559	6	CB258391	CB258391	30-E01108	
46	54	2.7	451	7	H76326	H76326	18031	Lambd
47	53	2.6	504	7	T43186	T43186	6449	Lambd
48	53	2.6	555	1	AV553768	AV553768	AV553768	
49	52	2.6	413	7	T76917	T76917	11695	Lambd
50	52	2.6	565	7	H76463	H76463	18168	Lambd
51	52	2.6	584	6	CB262297	CB262297	66-E8977-	
52	50	2.5	382	7	T42126	T42126	5389	Lambd
53	49	2.4	323	8	B2355348	B2355348	SALK_1266	
54	49	2.4	339	7	Z34671	Z34671	ATT3431.Ve	
55	46	2.4	434	7	T46309	T46309	9572	Lambd
56	46	2.3	208	7	T43549	T43549	6812	Lambd
57	45	2.2	361	7	W43089	W43089	22470	Lambd
58	45	2.2	412	6	CB258452	CB258452	06-E01108	
59	45	2.2	607	6	CB259904	CB259904	14-E9625-	
60	45	2.2	661	5	BP561200	BP561200	BP561200	
61	45	2.2	688	5	BU636599	BU636599	002A09.In	
62	45	2.2	693	2	BE038094	BE038094	AA08G09.A	
63	45	2.2	1522	3	CNS0A2Q2	CNS0A2Q2	AX827234	Arabidops
64	44	2.2	206	7	T45981	T45981	9244	Lambd
65	42	2.1	479	1	AA040988	AA040988	24254	CD4
66	40	2.0	434	7	T41751	T41751	10332	Lambd
67	38	1.9	413	7	T44572	T44572	7835	Lambd
68	37	1.8	257	7	T13996	T13996	2161	Lambd
C 69	34	1.7	713	8	BH439107	BH439107	BOHAK61TR	
C 70	31	1.5	474	6	CA963963	CA963963	CAT1008A0	
C 71	25	1.2	463	5	BW550940	BW550940	BW550940	
C 72	25	1.2	507	5	BW520746	BW520746	BW520746	
C 73	25	1.2	566	5	BW561732	BW561732	BW561732	
C 74	25	1.2	590	5	BW566410	BW566410	BW566410	
C 75	24	1.2	154	1	AI686081	AI686081	tw98f11.x	
C 76	24	1.2	196	1	AI627621	AI627621	ty18h01.x	
C 77	24	1.2	371	1	AI446538	AI446538	tj05c01.x	
C 78	24	1.2	435	6	BY696245	BY696245	BY696245	
C 79	24	1.2	448	8	CC051946	CC051946	CC051946	
C 80	24	1.2	451	5	BX783160	BX783160	BX783160	
C 81	24	1.2	457	8	BH253111	BH253111	SALK_0144	
C 82	24	1.2	461	9	CB633039	CB633039	tigt-g98-	
C 83	24	1.2	597	8	BH745927	BH745927	gzt7a08.b	
C 84	24	1.2	633	9	CG931470	CG931470	CG931470	
C 85	24	1.2	656	7	CK678882	CK678882	CK678882	
C 86	24	1.2	705	9	CE231251	CE231251	tigt-g98-	
C 87	24	1.2	720	8	BH994683	BH994683	oeK41C03.	
C 88	24	1.2	749	8	BZ062372	BZ062372	l1e85b02.	
C 89	24	1.2	786	8	BH425990	BH425990	BH425990	
C 90	24	1.2	837	9	AG480808	AG480808	AG480808	
C 91	24	1.2	961	7	CK230311	CK230311	ILLUMINIGEN	
C 92	24	1.2	2341	3	CR692849	CR692849	CR692849	
C 93	23	1.1	131	1	AL803019	AL803019	AL803019	
C 94	23	1.1	232	9	CR402810	CR402810	Arabidops	
C 95	23	1.1	238	1	AA682395	AA682395	z186c09.8	
C 96	23	1.1	276	5	BX746235	BX746235	BX746235	
C 97	23	1.1	300	1	AU113083	AU113083	AU113083	

98	23	1.1	300	1	AU115124	AU115124	171	23	1.1	1069	6	CD325027	CD325027	AGENCOURT
99	23	1.1	300	1	AU115813	AU115813	c 172	23	1.1	1425	9	AG320854	AG320854	Mus muscu
100	23	1.1	300	1	AU115864	AU115864	173	22	1.1	166	2	BE029931	BE029931	kp36908.y
101	23	1.1	300	1	AU116530	AU116530	c 174	22	1.1	185	9	CE538112	CE538112	tigr-g88-
102	23	1.1	300	6	C29544	C29544	175	22	1.1	191	6	CA341180	CA341180	haa80e05.
103	23	1.1	300	6	C32828	C32828	176	22	1.1	202	4	B1849732	B1849732	477657.MA
104	23	1.1	300	6	C57248	C57248	177	22	1.1	202	9	CL526039	CL526039	EY08717.D
105	23	1.1	300	6	C57422	C57422	178	22	1.1	225	5	BU844069	BU844069	AGENCOURT
106	23	1.1	300	6	C57691	C57691	179	22	1.1	227	5	BU960462	BU960462	AGENCOURT
107	23	1.1	344	1	AU211691	AU211691	180	22	1.1	230	4	B1746533	B1746533	rm28605.y
108	23	1.1	375	7	CR428049	CR428049	181	22	1.1	240	1	AU071654	AU071654	AU071654
109	23	1.1	425	8	BH173064	BH173064	182	22	1.1	240	1	AU072568	AU072568	AU072568
c 110	23	1.1	451	6	CB104242	CB104242	183	22	1.1	247	6	CA341165	CA341165	haa79g12.
111	23	1.1	519	4	BJ815455	BJ815455	184	22	1.1	249	6	CA739149	CA739149	wpi28.pk0
112	23	1.1	534	4	BJ144876	BJ144876	c 185	22	1.1	254	7	CN751112	CN751112	ApHL3SD-I
113	23	1.1	547	1	A1065346	A1065346	186	22	1.1	277	1	AV529773	AV529773	AV529773
114	23	1.1	548	4	BJ780148	BJ780148	187	22	1.1	279	9	AL766416	AL766416	Arabi408
115	23	1.1	555	4	BJ787272	BJ787272	188	22	1.1	290	1	AV848388	AV848388	AV848388
c 116	23	1.1	555	7	CF403324	CF403324	189	22	1.1	318	2	BF605181	BF605181	271463.MA
117	23	1.1	566	7	CK553471	CK553471	c 190	22	1.1	324	5	BW009825	BW009825	BW009825
118	23	1.1	574	1	AL643196	AL643196	191	22	1.1	325	7	CK721101	CK721101	tad50n03.
119	23	1.1	575	4	BJ815759	BJ815759	192	22	1.1	329	2	AV997486	AV997486	AV997486
120	23	1.1	576	4	BJ784050	BJ784050	193	22	1.1	351	1	AA226320	AA226320	nc20c08.s
121	23	1.1	577	1	AL797114	AL797114	194	22	1.1	361	4	BG226617	BG226617	kp91e06.y
122	23	1.1	587	1	AL651939	AL651939	195	22	1.1	362	2	BQ029053	BQ029053	KD24C04.y
123	23	1.1	596	4	BJ37599	BJ37599	196	22	1.1	381	8	BZ477447	BZ477447	BONEG26TF
124	23	1.1	597	8	BH830615	BH830615	c 197	22	1.1	388	8	BH490847	BH490847	BOGIN73TR
125	23	1.1	606	7	CO122794	CO122794	198	22	1.1	402	2	AW963923	AW963923	EST375996
c 126	23	1.1	612	8	BZ509657	BZ509657	199	22	1.1	406	6	CA758925	CA758925	OE12B10.T
127	23	1.1	615	4	BJ783834	BJ783834	200	22	1.1	423	1	AU226827	AU226827	AU226827
128	23	1.1	616	4	BJ786358	BJ786358	201	22	1.1	424	6	CB475298	CB475298	jne105.F0
c 129	23	1.1	616	6	CB534226	CB534226	202	22	1.1	425	4	BG019528	BG019528	daa21c04.
130	23	1.1	620	4	BJ776705	BJ776705	203	22	1.1	432	1	AU286777	AU286777	AU286777
c 131	23	1.1	627	7	CK947593	CK947593	c 204	22	1.1	457	2	AW235793	AW235793	xn22c12.x
132	23	1.1	629	4	BJ810742	BJ810742	c 205	22	1.1	468	6	BY701501	BY701501	BY701501
133	23	1.1	633	4	BJ792314	BJ792314	c 206	22	1.1	471	1	A1127091	A1127091	qb97g09.x
134	23	1.1	636	1	AL876013	AL876013	c 207	22	1.1	481	8	BH432980	BH432980	BOGLC85TF
135	23	1.1	636	4	BJ809769	BJ809769	c 208	22	1.1	485	7	CO132580	CO132580	GR_Eb45I
c 136	23	1.1	642	4	BJ810694	BJ810694	209	22	1.1	494	2	BE223219	BE223219	kp74b04.y
c 137	23	1.1	647	1	AL870755	AL870755	c 210	22	1.1	496	9	CL873214	CL873214	abe87c07.
138	23	1.1	647	1	AL891461	AL891461	211	22	1.1	503	7	CL574891	CL574891	OB_Ba002
139	23	1.1	648	4	BJ815372	BJ815372	212	22	1.1	508	7	CO118559	CO118559	GR_Bb020
c 140	23	1.1	650	9	CE612712	CE612712	213	22	1.1	508	2	BE580949	BE580949	kp83e01.y
c 141	23	1.1	658	8	BH560797	BH560797	214	22	1.1	511	1	AU021880	AU021880	AU021880
c 142	23	1.1	662	6	CB535472	CB535472	215	22	1.1	516	7	CO082017	CO082017	GR_Ea46G
143	23	1.1	671	4	BJ797903	BJ797903	216	22	1.1	532	8	AZ128327	AZ128327	OSUNB009
c 144	23	1.1	680	6	CB468000	CB468000	217	22	1.1	533	2	AW496614	AW496614	AW496614
c 145	23	1.1	685	6	CB438034	CB438034	c 218	22	1.1	541	8	AZ263258	AZ263258	RPCI-23-1
146	23	1.1	687	4	BJ782838	BJ782838	219	22	1.1	555	5	BP529839	BP529839	BP529839
147	23	1.1	695	1	AU213077	AU213077	220	22	1.1	560	7	CV465316	CV465316	taj26f10.
c 148	23	1.1	699	6	BY711080	BY711080	221	22	1.1	569	9	CC961362	CC961362	BOLEA44TR
c 149	23	1.1	705	9	CR824385	CR824385	222	22	1.1	578	7	CO073979	CO073979	GR_Ea33N
150	23	1.1	715	4	BJ794920	BJ794920	223	22	1.1	579	7	CO103660	CO103660	GR_Eb003
151	23	1.1	731	8	BH824376	BH824376	224	22	1.1	587	6	CA844825	CA844825	hab592b08.
152	23	1.1	738	2	BF578409	BF578409	225	22	1.1	604	5	BU495161	BU495161	PfESToab8
153	23	1.1	740	4	BJ154614	BJ154614	226	22	1.1	612	9	CNS040GM	CNS040GM	Tetraodon
154	23	1.1	756	7	CN168241	CN168241	c 227	22	1.1	613	9	CF657367	CF657367	tac74f11.
155	23	1.1	760	9	CS587124	CS587124	228	22	1.1	618	7	CF505946	CF505946	USDA-FP-1
156	23	1.1	767	7	CR580998	CR580998	229	22	1.1	623	9	CE470350	CE470350	tigr-g88-
157	23	1.1	777	5	BX698728	BX698728	230	22	1.1	627	8	BH559200	BH559200	BOGLJ38TR
c 158	23	1.1	786	7	CR564890	CR564890	231	22	1.1	631	8	BH685331	BH685331	BOMB49TR
159	23	1.1	798	5	BX718267	BX718267	232	22	1.1	649	8	AZ570242	AZ570242	272PvB06
160	23	1.1	799	8	BH477962	BH477962	233	22	1.1	651	8	BH987737	BH987737	oed09d04.
161	23	1.1	800	5	EX701238	EX701238	c 234	22	1.1	659	7	CN048526	CN048526	v2_pl14.e
162	23	1.1	802	5	BX695380	BX695380	235	22	1.1	665	8	BH524284	BH524284	BOGCC40TR
163	23	1.1	813	8	BH558385	BH558385	236	22	1.1	670	8	AZ573465	AZ573465	317PvG01
c 164	23	1.1	832	8	AZ193186	AZ193186	237	22	1.1	672	8	BH521070	BH521070	BOGGM57TF
165	23	1.1	839	9	AG542833	AG542833	c 238	22	1.1	675	8	BZ179662	BZ179662	CH230-484
c 166	23	1.1	855	7	CK196558	CK196558	239	22	1.1	680	9	CE252481	CE252481	tigr-g88-
c 167	23	1.1	860	7	CR583704	CR583704	c 240	22	1.1	692	8	BH513027	BH513027	BOHKK08TR
168	23	1.1	861	8	BZ509941	BZ509941	241	22	1.1	696	8	AZ985740	AZ985740	2M027M11
169	23	1.1	1002	9	CL029400	CL029400	242	22	1.1	702	7	CF654199	CF654199	tac74f11.
170	23	1.1	1043	9	CL057311	CL057311	243	22	1.1	704	8	BZ036699	BZ036699	oeh35h11.

244	1.1	706	9	CE018520	tigr-g88-	317	21	1.0	298	7	CO942307	CO942307 UMC-p2mm1
245	1.1	733	6	AG537867	Mus muscu	c 318	21	1.0	301	1	AA598032	AA598032 23281 Lam
246	1.1	736	6	CB947571	AGENCOURT	319	21	1.0	320	5	BP604656	BP604656 BP604656
247	1.1	736	6	AG441391	Mus muscu	320	21	1.0	325	7	CR514555	CR514555 CR514555
248	1.1	755	6	CB953185	AGENCOURT	321	21	1.0	327	1	AI944701	AI944701 bs04405.Y
249	1.1	762	8	BZ048147	kg33a04.	322	21	1.0	334	7	T00052	T00052 wEST00773.Z
250	1.1	764	8	CB2048147	t071020ba	323	21	1.0	341	4	BM159706	BM159706 EST562229
251	1.1	764	8	CC912524	CC912524	324	21	1.0	345	7	CN054664	CN054664 Salanade
252	1.1	770	8	BZ428252	BONP17TR	325	21	1.0	364	2	BF018792	BF018792 ux80109.X
253	1.1	774	9	AG537749	Mus muscu	c 326	21	1.0	370	9	CL376469	CL376469 RPC144.44
254	1.1	779	9	CE820835	tigr-g88-	327	21	1.0	370	9	CL376469	CL376469 RPC144.44
255	1.1	783	9	AG032294	Pan trogl	328	21	1.0	374	8	BM18961	BM18961 SALK_0400
256	1.1	788	8	BH945848	obu91e09.	329	21	1.0	377	6	CA819562	CA819562 salu80611.
257	1.1	791	8	BH588772	BOHLK81TR	330	21	1.0	386	1	AL790677	AL790677 AL790677
258	1.1	805	9	CG678715	CG678715	331	21	1.0	387	8	B31605	B31605 HS-1011-A2-
259	1.1	817	9	CR307559	Medicago	332	21	1.0	389	7	CO098817	CO098817 GR_Ea23F
260	1.1	820	8	BZ482438	BONLS89TR	c 333	21	1.0	397	6	BY701502	BY701502 BV701502
261	1.1	822	8	BH441162	BOGQL32TR	334	21	1.0	405	5	BP658043	BP658043 BP658043
262	1.1	824	5	BH842180	AGENCOURT	335	21	1.0	410	9	EX656137	EX656137 Arabidops
263	1.1	829	8	BZ478437	BONHR80TF	336	21	1.0	411	1	AU287295	AU287295 AU287295
264	1.1	838	8	BH657873	BH657873	337	21	1.0	415	2	BF406978	BF406978 UI-R-BJ2-
265	1.1	852	9	AG472015	Mus muscu	c 338	21	1.0	415	2	BM161558	BM161558 EST564081
266	1.1	854	7	CK161044	FGAS04271	339	21	1.0	422	8	BH117579	BH117579 RPC1-24-2
267	1.1	863	7	BF785633	AGENCOURT	340	21	1.0	424	4	BI276797	BI276797 UI-R-CX0-
268	1.1	867	4	CG309901	HVSMC001	341	21	1.0	424	8	BH248417	BH248417 BOGAG26TF
269	1.1	886	9	BZ434167	BONRD80TR	342	21	1.0	425	5	BM689801	BM689801 BX689801
270	1.1	890	9	CL067679	Medicago	343	21	1.0	427	2	AW084190	AW084190 xc48h03.X
271	1.1	891	9	CR318708	Medicago	344	21	1.0	433	5	BU757580	BU757580 UI-1-CF0-
272	1.1	892	4	BM358164	GA_Ea000	345	21	1.0	434	5	RG365016	RG365016 104797 MA
273	1.1	895	9	CG960097	MBEHE73TR	346	21	1.0	438	5	BQ892044	BQ892044 AGENCOURT
274	1.1	896	2	BE053710	GA_Ea003	347	21	1.0	447	5	BI083273	BI083273 602875192
275	1.1	904	9	CL481284	SATL_339	348	21	1.0	447	5	BQ031485	BQ031485 UI-1-CF0-
276	1.1	905	8	CC339924	OCQAK61TV	349	21	1.0	450	2	BF401454	BF401454 UI-R-CA0-
277	1.1	906	7	CR418027	CR418027	c 350	21	1.0	451	9	CE532700	CE532700 tigr-g88-
278	1.1	912	5	BU912884	AGENCOURT	351	21	1.0	454	1	AI475283	AI475283 t181c03.X
279	1.1	928	9	CL070690	CH216-119	352	21	1.0	454	5	BP587449	BP587449 BP587449
280	1.1	929	9	CL071159	CH216-120	353	21	1.0	464	9	CL874742	CL874742 abe98c10.
281	1.1	969	9	CG768497	TCB47.2.A	c 354	21	1.0	469	7	T93843	T93843 ye05f03.r1
282	1.1	997	9	CNS07CSZ	CL43593 T3 end of	355	21	1.0	489	7	BZ507738	BZ507738 BONNH55TR
283	1.1	998	9	CL066158	CH216-108	356	21	1.0	491	7	CO647252	CO647252 ILLUMIGEN
284	1.1	999	6	CD051186	AGENCOURT	c 357	21	1.0	491	8	CC459833	CC459833 SALK_1336
285	1.1	1005	4	BM801032	AGENCOURT	358	21	1.0	510	6	CB782711	CB782711 AMGNNUC:N
286	1.1	1019	8	CC268975	CH261-60D	359	21	1.0	513	1	AI716524	AI716524 UI-R-Y0-a
287	1.1	1043	9	CNS06CRL	T7 end of	360	21	1.0	516	5	BQ207626	BQ207626 UI-R-DY1-
288	1.1	1135	9	CL027221	CH216-25G	c 361	21	1.0	523	9	CL173698	CL173698 OR_BBA008
289	1.1	1190	3	CR672279	Tetraodon	c 362	21	1.0	529	6	BY593199	BY593199 BY593199
290	1.1	1196	9	AG346314	Mus muscu	c 363	21	1.0	531	1	AI442890	AI442890 sa28c03.X
291	1.1	1203	3	CR679028	Tetraodon	364	21	1.0	534	5	BM836397	BM836397 BX836397
292	1.1	1207	8	CC275232	CH261-931	c 365	21	1.0	538	1	AO611353	AO611353 HS_5088.B
293	1.1	1247	9	CG756067	P051-2-B0	366	21	1.0	539	1	AL914006	AL914006 AL914006
294	1.1	1289	9	CL016332	CH216-170	c 367	21	1.0	539	1	AL914006	AL914006 AG-ND-169
295	1.1	1300	9	CG754066	P049-2-E0	c 368	21	1.0	544	8	BH399346	BH399346 Medicago
296	1.1	1370	8	CC214165	CH261-177	369	21	1.0	547	9	CR348902	CR348902 Medicago
297	1.1	1402	9	CG750735	P045-2-B0	c 370	21	1.0	548	8	CC460022	CC460022 SALK_1384
298	1.1	1586	3	CR679862	Tetraodon	c 371	21	1.0	551	1	AU288092	AU288092 AU288092
299	1.0	109	7	CNS63166	CNS63166	c 372	21	1.0	556	8	AZ424325	AZ424325 IM0203F22
300	1.0	131	9	CR395843	Arabidops	c 373	21	1.0	561	4	BI804888	BI804888 S001F08.S
301	1.0	154	7	CK372788	la191901.	374	21	1.0	561	8	AO780691	AO780691 HS_3169.A
302	1.0	182	7	CO819074	CSECS124B	375	21	1.0	565	8	BH884121	BH884121 hw49h02_g
303	1.0	206	9	CE589497	tigr-g88-	376	21	1.0	571	8	BZ302233	BZ302233 KD1724.pl
304	1.0	214	5	BQ352247	RCO-HT077	377	21	1.0	587	8	B62592	B62592 T22G15TR.TA
305	1.0	218	4	BM161736	BM161736	c 378	21	1.0	589	1	AU288091	AU288091 AU288091
306	1.0	218	4	BM162558	BM162558	c 379	21	1.0	593	5	BU897943	BU897943 X072C12.P
307	1.0	218	4	BM170990	EST573513	c 380	21	1.0	605	7	CF372166	CF372166 CSCS049B
308	1.0	238	4	BM169266	EST571789	c 381	21	1.0	605	8	BX968527	BX968527 Forward.B
309	1.0	238	9	CC607455	OGQBR90TH	c 382	21	1.0	608	8	BH769531	BH769531 BMAC366D
310	1.0	242	4	BM166537	EST569060	383	21	1.0	616	9	AG589467	AG589467 Mus muscu
311	1.0	256	4	BM168436	EST570959	384	21	1.0	617	9	AW397173	AW397173 ag67g04.Y
312	1.0	274	1	AV139759	AV139759	385	21	1.0	617	9	CE351375	CE351375 tigr-g88-
313	1.0	274	2	BB343057	BB343057	c 386	21	1.0	630	7	CO083635	CO083635 GR_Ea48M
314	1.0	283	2	BF148282	uy84h03.X	387	21	1.0	630	7	CL807946	CL807946 OR_CBA002
315	1.0	291	1	AI412123	EST240417	388	21	1.0	630	9	BE821946	BE821946 GM7000016A
316	1.0	297	9	CC883632	SALK_0953	389	21	1.0	635	2	BE821946	BE821946 GM7000016A

C 536	1.0	1273	9	CL021453	CL021453	CH216-8G1	C 609	20	1.0	340	7	T89114	T89114	yc84hl2.e1
C 537	1.0	1280	9	CL080475	CL080475	CH216-158	C 610	20	1.0	343	2	BF392658	BF392658	UI-R-CA0-
C 538	1.0	1296	4	BM467347	BM467347	AGENCOURT	C 611	20	1.0	346	7	CK746829	CK746829	asm01-8mb
C 539	1.0	1307	8	CC238331	CC238331	CH261-192	C 612	20	1.0	353	7	CR585105	CR585105	CR585105
C 540	1.0	1378	9	CG744810	CG744810	P037-3-BO	C 613	20	1.0	358	4	BM093512	BM093512	8s109g11.
C 541	1.0	1467	9	AG276258	AG276258	Mus muscu	C 614	20	1.0	362	5	BQ265755	BQ265755	NISC-ff08
C 542	1.0	2348	3	AK082373	AK082373	Mus muscu	C 615	20	1.0	369	2	BE046033	BE046033	hd91h03.x
C 543	1.0	2927	3	AK035855	AK035855	Mus muscu	C 616	20	1.0	372	4	BG626208	BG626208	cc-eaficL
C 544	1.0	69	9	CR396216	CR396216	Arabidops	C 617	20	1.0	372	9	AG199023	AG199023	Pan trogl
C 545	1.0	109	7	CV286121	CV286121	tak66a03.	C 618	20	1.0	374	4	BI494148	BI494148	df108a08.
C 546	1.0	121	9	BX663279	BX663279	Arabidops	C 619	20	1.0	374	7	CR585106	CR585106	CR585106
C 547	1.0	137	9	CR271484	CR271484	Forward s	C 620	20	1.0	376	8	AQ031215	AQ031215	HS 2214.A
C 548	1.0	142	9	CR402516	CR402516	Arabidops	C 621	20	1.0	378	4	BQ273117	BQ273117	602296031
C 549	1.0	150	9	CG479469	CG479469	OST10324	C 622	20	1.0	382	6	CB477376	CB477376	jnr20.G07
C 550	1.0	154	1	AL898443	AL898443	AL898443	C 623	20	1.0	383	1	AI711079	AI711079	UI-R-AE1-
C 551	1.0	154	1	AU197517	AU197517	AU197517	C 624	20	1.0	384	6	CB352268	CB352268	ZF001-P00
C 552	1.0	155	9	BX652345	BX652345	Arabidops	C 625	20	1.0	385	5	BP506991	BP506991	BP506991
C 553	1.0	180	8	AZ023673	AZ023673	RFC1-23-3	C 626	20	1.0	385	8	BZ942645	BZ942645	CH240.93P
C 554	1.0	185	9	AG021707	AG021707	Oryza sat	C 627	20	1.0	387	6	CD447293	CD447293	E04912707
C 555	1.0	193	4	BG237554	BG237554	sab14b03.	C 628	20	1.0	388	1	AL387115	AL387115	MCBCA0E05
C 556	1.0	197	7	H74980	H74980	568 Random	C 629	20	1.0	388	8	AZ513003	AZ513003	1M0358K23
C 557	1.0	199	8	BH619074	BH619074	SALK_0402	C 630	20	1.0	388	8	BZ176141	BZ176141	CH230-397
C 558	1.0	201	6	CB818268	CB818268	abl22pz.r	C 631	20	1.0	389	1	AI968124	AI968124	wul3d07.x
C 559	1.0	205	4	BI743670	BI743670	kx50d01.y	C 632	20	1.0	391	1	AV816635	AV816635	AV816635
C 560	1.0	207	9	CR402515	CR402515	Arabidops	C 633	20	1.0	391	4	BI183288	BI183288	UNL-P-FN-
C 561	1.0	212	4	EJ051349	EJ051349	EJ051349	C 634	20	1.0	393	1	AI603431	AI603431	UI-R-AC1-
C 562	1.0	216	2	BF223998	BF223998	7q36e06.x	C 635	20	1.0	398	1	AA576018	AA576018	nm57d05.8
C 563	1.0	216	2	AW025767	AW025767	wu06h07.x	C 636	20	1.0	401	5	BQ297712	BQ297712	8ac01f04.
C 564	1.0	216	2	BE672366	BE672366	7a56f06.x	C 637	20	1.0	401	6	CA150676	CA150676	SCBFR2204
C 565	1.0	220	9	CE496100	CE496100	tigr-gss-	C 638	20	1.0	402	1	AU182665	AU182665	AU182665
C 566	1.0	221	2	AW196585	AW196585	xm35b01.x	C 639	20	1.0	403	8	AZ155885	AZ155885	SP_0051.B
C 567	1.0	223	9	AL771927	AL771927	Arabidops	C 640	20	1.0	404	8	BZ696711	BZ696711	SP_Ba008
C 568	1.0	224	5	BQ834098	BQ834098	Arabidops	C 641	20	1.0	405	8	AQ494596	AQ494596	HS_5171.B
C 569	1.0	224	9	CE397193	CE397193	tigr-gss-	C 642	20	1.0	406	1	AI869663	AI869663	wu02b01.x
C 570	1.0	226	9	CE397193	CE397193	Danio rer	C 643	20	1.0	411	2	BE603878	BE603878	CS72.GS.L
C 571	1.0	228	9	CR43B14S	CR43B14S	C99469	C 644	20	1.0	414	6	BY666701	BY666701	BY666701
C 572	1.0	229	6	D99469	D99469	C99469	C 645	20	1.0	416	2	BF407098	BF407098	UI-R-BJ2-
C 573	1.0	229	6	CK088013	CK088013	A031P27.3	C 646	20	1.0	417	7	CV296543	CV296543	ESTP884920
C 574	1.0	248	7	CNS76214	CNS76214	rc25g12.x	C 647	20	1.0	417	7	CV296543	CV296543	ESTP884920
C 575	1.0	249	7	CNS75099	CNS75099	01013AAR	C 648	20	1.0	418	4	BI745271	BI745271	rc598d02.y
C 576	1.0	251	1	AV377096	AV377096	AV377096	C 649	20	1.0	418	4	BI745271	BI745271	rc598d02.y
C 577	1.0	251	1	AI717221	AI717221	UI-R-Y0-a	C 650	20	1.0	419	1	AI142921	AI142921	OZ45d08.x
C 578	1.0	256	2	AW312154	AW312154	6438 MARC	C 651	20	1.0	419	8	BE103078	BE103078	UI-R-BX0-
C 579	1.0	256	2	AW312155	AW312155	6439 MARC	C 652	20	1.0	419	8	AZ657284	AZ657284	1M0533E24
C 580	1.0	256	2	BE941680	BE941680	EST421259	C 653	20	1.0	420	1	AI637665	AI637665	tt10908.x
C 581	1.0	256	6	CB476876	CB476876	jnr13_B07	C 654	20	1.0	421	4	BM285549	BM285549	UI-R-DK0-
C 582	1.0	256	9	AL771928	AL771928	Arabidops	C 655	20	1.0	421	4	BM285549	BM285549	524207.MA
C 583	1.0	262	2	BE063882	BE063882	QV3-BT029	C 656	20	1.0	421	8	BH239686	BH239686	ATCD90TR
C 584	1.0	262	8	AZ617225	AZ617225	1M0448H23	C 657	20	1.0	424	5	BQ451056	BQ451056	PFESt0ab0
C 585	1.0	269	4	BJ329492	BJ329492	BJ329492	C 658	20	1.0	424	5	BQ451056	BQ451056	PFESt0ab0
C 586	1.0	270	2	BB116721	BB116721	BB116721	C 659	20	1.0	424	8	AQ353154	AQ353154	CITBI-E1-
C 587	1.0	276	1	AL387116	AL387116	MCBCA0E05	C 660	20	1.0	426	5	BP636662	BP636662	BY549355
C 588	1.0	279	1	AA841756	AA841756	MB3D6V6H0	C 661	20	1.0	426	5	BP636662	BP636662	BY549355
C 589	1.0	280	2	AW535862	AW535862	UI-R-B50-	C 662	20	1.0	427	7	CV266036	CV266036	WS02028.B
C 590	1.0	286	1	AV228951	AV228951	AV228951	C 663	20	1.0	429	7	CV266036	CV266036	WS02028.B
C 591	1.0	290	1	AV296330	AV296330	AV296330	C 664	20	1.0	429	8	CC051276	CC051276	SALK_0042
C 592	1.0	292	5	BU497621	BU497621	PFESt0ab8	C 665	20	1.0	430	7	CN77518	CN77518	taf64904.
C 593	1.0	292	7	CR473140	CR473140	CR473140	C 666	20	1.0	430	9	CE094776	CE094776	tigr-g8B-
C 594	1.0	293	4	BI276358	BI276358	UI-R-CW0-	C 667	20	1.0	430	9	CE094776	CE094776	tigr-g8B-
C 595	1.0	293	5	BM958593	BM958593	PLATE_6_E	C 668	20	1.0	431	1	AA976171	AA976171	on33e03.8
C 596	1.0	294	9	CL655629	CL655629	PR10124a	C 669	20	1.0	435	2	BB357604	BB357604	BR357604
C 597	1.0	296	8	AQ892801	AQ892801	HS_3156.B	C 670	20	1.0	435	6	BY697059	BY697059	BY697059
C 598	1.0	298	8	B2822871	B2822871	UI-R-C2-n	C 671	20	1.0	436	1	BI450200	BI450200	da676c11.
C 599	1.0	308	1	AI071417	AI071417	UI-FUHU3TD	C 672	20	1.0	437	8	AQ842304	AQ842304	AV548729
C 600	1.0	308	1	AI307315	AI307315	tb18h02.x	C 673	20	1.0	438	4	BM264824	BM264824	AV548729
C 601	1.0	315	7	CN777266	CN777266	taf64904.	C 674	20	1.0	438	8	AZ438702	AZ438702	FW62h10.x
C 602	1.0	316	1	AV340139	AV340139	AV340139	C 675	20	1.0	439	2	BF394433	BF394433	1M0228J21
C 603	1.0	320	6	CA998835	CA998835	S234J_G12	C 676	20	1.0	442	1	AJ555592	AJ555592	UI-R-CA0-
C 604	1.0	328	1	AL718854	AL718854	AL718854	C 677	20	1.0	442	6	CB967127	CB967127	AJ555592
C 605	1.0	335	1	AL718792	AL718792	AL718792	C 678	20	1.0	446	1	AL970529	AL970529	NL48_F02
C 606	1.0	337	7	CF226888	CF226888	EST1891.T	C 679	20	1.0	446	5	BM517688	BM517688	AL970529
C 607	1.0	339	6	CA761783	CA761783	BR060013A	C 680	20	1.0	448	1	AU094162	AU094162	BM517688
C 608	1.0	340	6	BY589623	BY589623	BY589623	C 681	20	1.0	449	2	AW469597	AW469597	hd29h06.x

682	20	1.0	450	2	BE503983	BE0603983	CS323-T7	755	20	1.0	514	1	AA646426	AA646426
683	20	1.0	450	4	BM089881	BM089881	503743 MA	c 756	20	1.0	514	1	AA890379	AA890379
c 684	20	1.0	450	8	AZ614923	AZ614923	1M0443P24	c 757	20	1.0	516	1	AI071451	AI071451
685	20	1.0	451	5	BUS32846	BUS32846	AGENCOURT	c 758	20	1.0	518	5	BX518489	BX518489
c 686	20	1.0	453	8	AZ147446	AZ147446	SP 0051 B	c 759	20	1.0	520	6	CD286777	CD286777
c 687	20	1.0	453	8	AZ2766006	AZ2766006	1M0563G15	c 760	20	1.0	520	8	BZ645682	BZ645682
688	20	1.0	455	1	AI607657	AI607657	VK52810.Y	c 761	20	1.0	522	4	BG374337	BG374337
c 689	20	1.0	455	7	CO106500	CO106500	GR_EB003	c 762	20	1.0	522	4	BJ087840	BJ087840
c 690	20	1.0	456	7	R41674	R41674	Yf96C10.s1	c 763	20	1.0	522	4	CF331346	CF331346
691	20	1.0	458	6	BY590498	BY590498	GR_EB004	c 764	20	1.0	523	8	AQ216493	AQ216493
692	20	1.0	458	7	CO110361	CO110361	GR_EB004	c 765	20	1.0	528	1	AU238852	AU238852
693	20	1.0	458	7	CO131930	CO131930	GR_EB44H	c 766	20	1.0	528	8	AQ423245	AQ423245
c 694	20	1.0	461	1	AI803878	AI803878	EP30811.X	c 767	20	1.0	529	5	BU873155	BU873155
c 695	20	1.0	461	2	BF514567	BF514567	UI-H-BW1-	c 768	20	1.0	529	6	CD812889	CD812889
c 696	20	1.0	462	1	AI263871	AI263871	Q108C02.X	c 769	20	1.0	529	7	CO093655	CO093655
697	20	1.0	463	7	CF536105	CF536105	UI-M-G10-	c 770	20	1.0	530	3	AK020140	AK020140
c 698	20	1.0	464	5	BX074618	BX074618	UNL-P-FN-	771	20	1.0	532	5	BX719469	BX719469
c 699	20	1.0	465	4	BI183996	BI183996	UNL-P-FN-	772	20	1.0	533	9	CL605701	CL605701
c 700	20	1.0	465	8	BH740202	BH740202	GF27A06.b	c 773	20	1.0	534	1	AL673936	AL673936
701	20	1.0	465	8	BZ645673	BZ645673	OGAN15TC	c 774	20	1.0	535	1	AL899290	AL899290
c 702	20	1.0	466	1	AI263875	AI263875	Q108C08.X	c 775	20	1.0	539	1	AL914099	AL914099
c 703	20	1.0	466	2	AM099311	AM099311	6D3B08.Y	c 776	20	1.0	539	1	AV591376	AV591376
704	20	1.0	466	5	BM958962	BM958962	PLATE 17	c 777	20	1.0	542	2	BE567770	BE567770
705	20	1.0	467	6	CD843533	CD843533	RFQ2_132J	c 778	20	1.0	542	7	CF361485	CF361485
c 706	20	1.0	467	2	AM099320	AM099320	6D3B08.Y	c 779	20	1.0	543	5	BX094920	BX094920
c 707	20	1.0	469	2	AM099340	AM099340	BY592340	c 780	20	1.0	543	6	BY719389	BY719389
c 708	20	1.0	471	8	BZ498830	BZ498830	BONOQ56TR	781	20	1.0	545	2	AM979392	AM979392
c 709	20	1.0	472	1	AL382713	AL382713	MLBC09E08	782	20	1.0	547	9	AG253109	AG253109
c 710	20	1.0	472	6	CD099530	CD099530	AGENCOURT	783	20	1.0	550	2	AM937930	AM937930
c 711	20	1.0	472	7	R60731	R60731	YH02d12.s1	784	20	1.0	551	7	CF258587	CF258587
c 712	20	1.0	473	9	CT939351	CT939351	SALK 0390	c 785	20	1.0	552	9	CE334517	CE334517
c 713	20	1.0	474	2	BE996388	BE996388	UI-M-CG0p	c 786	20	1.0	554	9	CE943392	CE943392
c 714	20	1.0	474	5	BX073418	BX073418	EX073418	787	20	1.0	555	5	BU544970	BU544970
c 715	20	1.0	476	2	BE570498	BE570498	601328611	788	20	1.0	557	5	BX686902	BX686902
c 716	20	1.0	476	5	BM958982	BM958982	PLATE 12	789	20	1.0	557	7	W56136	W56136
c 717	20	1.0	476	1	CG262481	CG262481	tae99C10-	790	20	1.0	560	2	BF042278	BF042278
c 718	20	1.0	476	9	CR311246	CR311246	Medicago	c 791	20	1.0	560	6	CA302655	CA302655
c 719	20	1.0	477	6	CB491154	CB491154	omykrtCHO	c 792	20	1.0	560	7	CO584415	CO584415
c 720	20	1.0	478	2	AM085982	AM085982	xc76604.X	793	20	1.0	561	9	CRI36705	CRI36705
721	20	1.0	479	5	BP051907	BP051907	BP051907	794	20	1.0	561	5	BX684839	BX684839
c 722	20	1.0	479	9	AG472666	AG472666	mus muscu	c 795	20	1.0	561	6	CF072720	CF072720
c 723	20	1.0	482	9	AG472666	AG472666	mus muscu	796	20	1.0	564	2	BF044226	BF044226
c 724	20	1.0	484	7	CO132557	CO132557	GR_EB45H	c 797	20	1.0	567	2	AM299392	AM299392
c 725	20	1.0	486	6	BY596595	BY596595	BY596595	c 798	20	1.0	567	8	AZ221188	AZ221188
726	20	1.0	489	2	BF769506	BF769506	RC3-IT001	799	20	1.0	567	8	BZ930601	BZ930601
c 727	20	1.0	490	6	CD332005	CD332005	StrPU537.	c 800	20	1.0	568	7	CF122111	CF122111
728	20	1.0	492	1	AI452197	AI452197	mp84611.X	801	20	1.0	570	5	BF769698	BF769698
c 729	20	1.0	492	6	CB083106	CB083106	hn66d10.b	c 802	20	1.0	574	9	CE298618	CE298618
c 730	20	1.0	493	2	BE224434	BE224434	kp62h09.Y	c 803	20	1.0	576	9	CR309991	CR309991
731	20	1.0	494	6	CB083022	CB083022	hn65C01.9	804	20	1.0	577	8	AZ406055	AZ406055
732	20	1.0	495	1	AL801009	AL801009	AL801009	c 805	20	1.0	580	5	BF507014	BF507014
733	20	1.0	495	8	AQ411068	AQ411068	HS_5064_B	c 806	20	1.0	580	8	AZ791848	AZ791848
c 734	20	1.0	496	4	BG346851	BG346851	dad16d11.	c 807	20	1.0	581	8	BH103608	BH103608
735	20	1.0	497	7	CG262761	CG262761	tae99C10.	c 808	20	1.0	582	7	CK958495	CK958495
c 736	20	1.0	498	1	AI479179	AI479179	tn55C10.X	c 809	20	1.0	582	7	CK968017	CK968017
c 737	20	1.0	498	8	BH066989	BH066989	ee62B05.X	c 810	20	1.0	583	6	CB427810	CB427810
c 738	20	1.0	500	1	AM086892	AM086892	AU086892	c 811	20	1.0	583	7	CF325019	CF325019
739	20	1.0	500	4	BI879983	BI879983	fm68C02.X	c 812	20	1.0	584	2	AM360909	AM360909
740	20	1.0	500	4	BJ675490	BJ675490	BJ675490	c 813	20	1.0	587	6	CD318251	CD318251
c 741	20	1.0	500	9	TA62G04P	TA62G04P	T_brucel	814	20	1.0	588	5	BU549164	BU549164
c 742	20	1.0	500	9	CL886197	CL886197	abf77f03.	c 815	20	1.0	589	7	CO113436	CO113436
c 743	20	1.0	502	4	BG934838	BG934838	353194 MA	c 816	20	1.0	590	1	AL797531	AL797531
744	20	1.0	503	1	AI744470	AI744470	WF89F08.X	c 817	20	1.0	590	4	BM565472	BM565472
745	20	1.0	505	4	BM027094	BM027094	G1T000038	c 818	20	1.0	590	9	CE451120	CE451120
746	20	1.0	505	5	BW561401	BW561401	BM561401	819	20	1.0	591	1	AL792316	AL792316
c 747	20	1.0	505	7	CK344316	CK344316	K0940A04-	c 747	20	1.0	593	4	BM492005	BM492005
748	20	1.0	506	4	BM705670	BM705670	UI-E-DX0-	c 821	20	1.0	594	1	AL866273	AL866273
749	20	1.0	508	1	AI517100	AI517100	GH27734.3	c 822	20	1.0	594	7	CK905543	CK905543
c 750	20	1.0	508	8	BH036716	BH036716	RPCI-24-3	c 823	20	1.0	595	8	AZ350172	AZ350172
c 751	20	1.0	509	8	BZ301321	BZ301321	KD1204.q1	824	20	1.0	598	4	BI065145	BI065145
c 752	20	1.0	510	4	BG581041	BG581041	EST482770	825	20	1.0	598	8	BZ936485	BZ936485
753	20	1.0	512	9	CE589403	CE589403	tigr-g88-	c 826	20	1.0	598	9	CE962093	CE962093
c 754	20	1.0	513	8	AZ245548	AZ245548	RPCI-23-5	c 827	20	1.0	600	9	CE600552	CE600552

C 828	20	1.0	603	7	CNI181526	CNI181526	UCRCS04_0	901	20	1.0	681	6	CB642315	CB642315	OSJNEB02H
C 829	20	1.0	608	9	CR833670	CR833670	GF0AAA67B	902	20	1.0	681	8	BH328780	BH328780	CH230-124
C 830	20	1.0	611	6	CB580439	CB580439	ANGNUC.U	C 903	20	1.0	682	5	BX771399	BX771399	BX771399
C 831	20	1.0	612	6	CB480349	CB480349	Jns63_A11	C 904	20	1.0	682	6	CA447127	CA447127	UI-H-AE10-
C 832	20	1.0	613	5	BW365651	BW365651	BW365651	C 905	20	1.0	682	7	CR845142	CR845142	UI-H-AE1-
C 833	20	1.0	614	1	AL797544	AL797544	AL797544	C 906	20	1.0	682	9	CR502176	CR502176	Medicago
C 834	20	1.0	614	4	BJ091667	BJ091667	BJ091667	C 907	20	1.0	685	1	AA141081	AA141081	CK01129.3
C 835	20	1.0	614	7	CK966903	CK966903	4082225_B	C 908	20	1.0	687	9	AG355801	AG355801	Mus muscu
C 836	20	1.0	614	9	CL745355	CL745355	OR_BBA008	C 909	20	1.0	692	8	BH949290	BH949290	odi83d11.
C 837	20	1.0	615	8	BZ430345	BZ430345	BONBO411R	C 910	20	1.0	695	8	AZ262461	AZ262461	RPCI-23-1
C 838	20	1.0	616	5	BQ206711	BQ206711	UI-R-DZ1-	C 911	20	1.0	697	4	BM410800	BM410800	EST585127
C 839	20	1.0	616	5	BU782721	BU782721	in08d12.x	C 912	20	1.0	697	8	BZ028293	BZ028293	OS93802.
C 840	20	1.0	616	7	CK980507	CK980507	4112401_B	C 913	20	1.0	701	6	CA761678	CA761678	BR060012A
C 841	20	1.0	616	7	CR588487	CR588487	FR588487	C 914	20	1.0	701	7	CF362790	CF362790	830581_MA
C 842	20	1.0	616	9	CR833828	CR833828	GR0AA67C	C 915	20	1.0	701	8	BH712624	BH712624	BOMIH69TR
C 843	20	1.0	616	9	CE217647	CE217647	tigr-g8s-	C 916	20	1.0	703	7	CF998252	CF998252	AGENCOURT
C 844	20	1.0	617	8	BH699669	BH699669	BOMQ75TF	C 917	20	1.0	703	7	CR576724	CR576724	CF576724
C 845	20	1.0	617	8	CK753882	CK753882	pam01-8ms	C 918	20	1.0	703	8	BH998456	BH998456	OH25d12.
C 846	20	1.0	622	7	CO209925	CO209925	WS00916.B	C 919	20	1.0	703	8	AZ481714	AZ481714	Mus muscu
C 847	20	1.0	623	7	CK373649	CK373649	la15ld02.	C 920	20	1.0	704	7	AG516727	AG516727	Mus muscu
C 848	20	1.0	626	5	BX777758	BX777758	EX777758	C 921	20	1.0	704	7	CNO67224	CNO67224	I21_Ag2_P
C 849	20	1.0	627	8	BZ945601	BZ945601	CH240_122	C 922	20	1.0	707	5	BX770361	BX770361	BX770361
C 850	20	1.0	628	8	AZ564995	AZ564995	203PWB12	C 923	20	1.0	707	8	BZ003972	BZ003972	osm73f12.
C 851	20	1.0	630	7	CR415803	CR415803	RP415803	C 924	20	1.0	708	4	BM119938	BM119938	L0932G11-
C 852	20	1.0	630	8	AQ584316	AQ584316	RP415803	C 925	20	1.0	708	4	BM119938	BM119938	L0932G11-
C 853	20	1.0	632	4	BG711626	BG711626	pglin.pk0	C 926	20	1.0	709	2	BBS34589	BBS34589	BBS34589
C 854	20	1.0	632	7	CO100067	CO100067	GR_Ea25E	C 927	20	1.0	710	8	BZ360976	BZ360976	CH230-374
C 855	20	1.0	634	6	CD450791	CD450791	USDA-FP1	C 928	20	1.0	710	8	AG046528	AG046528	Pan trogl
C 856	20	1.0	638	8	BH032524	BH032524	RP415803	C 929	20	1.0	713	9	AG184635	AG184635	Pan trogl
C 857	20	1.0	639	6	CB321360	CB321360	AGENCOURT	C 930	20	1.0	715	9	AG328370	AG328370	Mus muscu
C 858	20	1.0	639	9	CE413718	CE413718	tigr-g8s-	C 931	20	1.0	715	9	AG328370	AG328370	Mus muscu
C 859	20	1.0	639	9	CE772212	CE772212	tigr-g8s-	C 932	20	1.0	718	7	CK629199	CK629199	AM3-AA001
C 860	20	1.0	641	4	BI113911	BI113911	602860757	C 933	20	1.0	718	8	CK629199	CK629199	AM3-AA001
C 861	20	1.0	641	4	BM385583	BM385583	UI-R-DM1-	C 934	20	1.0	720	1	AJ449315	AJ449315	AG328370
C 862	20	1.0	641	9	CE528122	CE528122	tigr-g8s-	C 935	20	1.0	720	5	BX704206	BX704206	Mus muscu
C 863	20	1.0	643	4	BG711553	BG711553	pglin.pk0	C 936	20	1.0	720	7	CK843162	CK843162	UI-R-Bu2-
C 864	20	1.0	643	8	AQ995413	AQ995413	RP415803	C 937	20	1.0	721	5	BQ194634	BQ194634	hpg3d10.b
C 865	20	1.0	644	4	BJ055200	BJ055200	BJ055200	C 938	20	1.0	721	5	BQ194634	BQ194634	UI-R-CN1-
C 866	20	1.0	644	8	BH406558	BH406558	GS078_Chi	C 939	20	1.0	722	8	BS124556	BS124556	BOGLI43TR
C 867	20	1.0	644	9	AG120072	AG120072	Pan trogl	C 940	20	1.0	722	7	CR411022	CR411022	CR411022
C 868	20	1.0	647	9	BX218216	BX218216	Danio rer	C 941	20	1.0	723	9	CL512761	CL512761	SAIL_866
C 869	20	1.0	647	7	CK134825	CK134825	RH03584.3	C 942	20	1.0	723	9	CL512761	CL512761	SAIL_866
C 870	20	1.0	649	2	BBS90438	BBS90438	BBS90438	C 943	20	1.0	724	5	BX504425	BX504425	DKF2p868B
C 871	20	1.0	649	7	CK967605	CK967605	4083058_B	C 944	20	1.0	725	6	CA785217	CA785217	8au26c12.
C 872	20	1.0	649	7	CO899673	CO899673	MdbdS019K	C 945	20	1.0	726	6	CB424405	CB424405	598653_MA
C 873	20	1.0	653	7	CF177174	CF177174	805629_MA	C 946	20	1.0	727	5	BU934070	BU934070	AGENCOURT
C 874	20	1.0	653	7	CK781454	CK781454	UI-M-GV0-	C 947	20	1.0	727	9	CE687482	CE687482	tigr-g8s-
C 875	20	1.0	655	1	AL853701	AL853701	AL853701	C 948	20	1.0	729	8	BH658246	BH658246	AG3558931
C 876	20	1.0	655	9	CG942594	CG942594	MBFR33TF	C 949	20	1.0	729	9	AG3558931	AG3558931	Mus muscu
C 877	20	1.0	655	9	CG942594	CG942594	MBFR33TF	C 950	20	1.0	731	5	BM444433	BM444433	Forward_B
C 878	20	1.0	656	2	BH636044	BH636044	MB636044	C 951	20	1.0	732	5	BM444433	BM444433	BM444433
C 879	20	1.0	656	6	CA282931	CA282931	SCGSD104	C 952	20	1.0	732	9	CR313144	CR313144	Medicago
C 880	20	1.0	659	8	AZ524926	AZ524926	238PDA11	C 953	20	1.0	736	5	EX694994	EX694994	Medicago
C 881	20	1.0	659	9	CR346516	CR346516	Medicago	C 954	20	1.0	736	5	CO556727	CO556727	AGENCOURT
C 882	20	1.0	660	6	CB680119	CB680119	OSJNEF04H	C 955	20	1.0	738	8	AQ956567	AQ956567	LEF74C06.
C 883	20	1.0	660	7	CR421580	CR421580	CR421580	C 956	20	1.0	738	8	BZ076742	BZ076742	IKF74C06.
C 884	20	1.0	661	1	AV398257	AV398257	AV398257	C 957	20	1.0	743	4	BG114327	BG114327	602286095
C 885	20	1.0	661	9	CE772978	CE772978	tigr-g8s-	C 958	20	1.0	743	5	BP713370	BP713370	BP713370
C 886	20	1.0	662	5	BQ224081	BQ224081	AGENCOURT	C 959	20	1.0	743	8	BH691702	BH691702	BOHWT1TR
C 887	20	1.0	663	7	CO083128	CO083128	GR_Ea48A	C 960	20	1.0	744	9	CR148154	CR148154	Forward_B
C 888	20	1.0	664	8	BH987748	BH987748	oeQ09A09.	C 961	20	1.0	744	9	CL096966	CL096966	ISB1-29B2
C 889	20	1.0	665	9	CL332927	CL332927	CH242_12J	C 962	20	1.0	745	6	CA464725	CA464725	AGENCOURT
C 890	20	1.0	666	4	BG478099	BG478099	60252742	C 963	20	1.0	745	6	CB942485	CB942485	AGENCOURT
C 891	20	1.0	666	8	BZ522003	BZ522003	BOKAE35TF	C 964	20	1.0	745	9	CL6113974	CL6113974	OR_BBA000
C 892	20	1.0	666	9	CE247436	CE247436	tigr-g8s-	C 965	20	1.0	746	8	AQ313807	AQ313807	RP415801
C 893	20	1.0	666	9	CE454006	CE454006	tigr-g8s-	C 966	20	1.0	747	5	BU120103	BU120103	603142345
C 894	20	1.0	669	9	AG049122	AG049122	Pan trogl	C 967	20	1.0	748	4	BG786069	BG786069	SEADMCO06
C 895	20	1.0	670	8	AZ269616	AZ269616	RP415803	C 968	20	1.0	752	9	CL865567	CL865567	t493b6.f
C 896	20	1.0	675	7	CK833299	CK833299	4057202_B	C 969	20	1.0	753	8	AQ858300	AQ858300	nbob0012K
C 897	20	1.0	679	8	AQ641944	AQ641944	RP415803	C 970	20	1.0	753	8	BH435311	BH435311	BOGOT07TR
C 898	20	1.0	680	8	BH953535	BH953535	odi84C02.	C 971	20	1.0	753	9	CG257171	CG257171	OGFES27H
C 899	20	1.0	680	9	AG290384	AG290384	Mus muscu	C 972	20	1.0	753	9	CG353925	CG353925	OGFA162TH
C 900	20	1.0	681	2	AW668077	AW668077	GA_Ea001	C 973	20	1.0	754	7	CO045126	CO045126	UI-M-GV0-

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c 974      20      1.0      754      8      BH239648      BH239648      ATYCD31TF
c 975      20      1.0      755      7      CO978928      CO978928      GM89003AI
c 976      20      1.0      757      5      BX754049      BX754049      BX754049
c 977      20      1.0      757      8      BH239301      BH239301      ATYCI23TF
c 978      20      1.0      760      6      CB595511      CB595511      AGENCOURT
c 979      20      1.0      760      9      CT734960      CT734960      OGLAR55TV
c 980      20      1.0      761      5      BU278802      BU278802      603864138
c 981      20      1.0      761      5      BU300818      BU300818      603609194
c 982      20      1.0      762      9      CL724848      CL724848      OR_BBA005
c 983      20      1.0      763      7      CR566567      CR566567      CR566567
c 984      20      1.0      764      9      AG607379      AG607379      Mus muscu
c 985      20      1.0      765      9      AG536282      AG536282      Mus muscu
c 986      20      1.0      766      9      CG023063      CG023063      ZMMBBC055
c 987      20      1.0      768      5      BU222878      BU222878      603947704
c 988      20      1.0      768      5      BU361683      BU361683      603784680
c 989      20      1.0      768      8      BH247726      BH247726      BOGAV42TF
c 990      20      1.0      769      1      AU003144      AU003144      AU003144
c 991      20      1.0      770      8      BH660017      BH660017      BOHSM12TR
c 992      20      1.0      771      5      BU435916      BU435916      603256958
c 993      20      1.0      773      7      CV266016      CV266016      WS02028.B
c 994      20      1.0      773      8      BZ062799      BZ062799      11f46f11.
c 995      20      1.0      774      4      BG936566      BG936566      SS1-M-GVO-
c 996      20      1.0      774      7      CO045108      CO045108      UI-M-GVO-
c 997      20      1.0      776      8      AZ667747      AZ667747      ENTFA51TF
c 998      20      1.0      778      8      BH238347      BH238347      ATYCF80TF
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ALIGNMENTS

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RESULT 1
CC796106/c      426 bp      DNA      linear      GSS      01-JUL-2003
LOCUS      SALK_092802.55.75 x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_092802.55.75.x, genomic
survey sequence.
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CC796106
CC796106.1      GI:32391329
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 426)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g20250.
Class: TDNA tagged.
Location/Qualifiers
1. .426
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/clone="SALK_092802.55.75.x"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
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elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Query Match      21.0%; Score 426; DB 9; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e-189; Indels 0; Gaps 0;
Matches 426; Conservative 0; Mismatches 0;

QY      153      TAAATTATCTATTTTATCAAAAGTTTGGTTTTAGGAAAAATGTATCTTTTCATATAAAAA 212
DB      426      TAAATTATCTATTTTATCAAAAGTTTGGTTTTAGGAAAAATGTATCTTTTCATATAAAAA 367

QY      213      ATATATAGATCTTCAAGAAACTGAATTTGGGTTTCACTATTTTATCGTTTGACACTAC 272
DB      366      ATATATAGATCTTCAAGAAACTGAATTTGGGTTTCACTATTTTATCGTTTGACACTAC 307

QY      273      TTTGACTTATCAAAAGAGTTTCAAAATAGAAAATAGAAATCAATCACACGTTTTCAGTGT 332
DB      306      TTTGACTTATCAAAAGAGTTTCAAAATAGAAAATAGAAATCAATCACACGTTTTCAGTGT 247

QY      333      AAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTTGTGTTTGTGTTTTCCTCAATCTG 392
DB      246      AAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTTGTGTTTGTGTTTTCCTCAATCTG 187

QY      393      CATGTTTTTTCGTTCCGTTGAACCAATTTCAACACTTTGTATATAACCGAATAGTATATA 452
DB      186      CATGTTTTTTCGTTCCGTTGAACCAATTTCAACACTTTGTATATAACCGAATAGTATATA 127

QY      453      CTAGACGTACGCCAATACCAAAATATAAAATCAAACTCAATTCACAAATTTGAATCTTACAC 512
DB      126      CTAGACGTACGCCAATACCAAAATATAAAATCAAACTCAATTCACAAATTTGAATCTTACAC 67

QY      513      CATATCATGCATATATATATATATATATATATATATATATATATATATATATATATATAT 572
DB      66      CATATCATGCATATATATATATATATATATATATATATATATATATATATATATATATAT 7

QY      573      AATATC 578
DB      6      AATATC 1

RESULT 2
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LOCUS      LERFK31TF LERA Arabidopsis thaliana genomic clone LERFK31, genomic
DEFINITION      survey sequence.
ACCESSION      AQ961292
VERSION      AQ961292.1      GI:6788993
KEYWORDS      GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 679)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T.,
Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atcigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TF
Class: shotgun.
Location/Qualifiers

FEATURES
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERFK31"
/clone_lib="LERA"
/notes="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."

ORIGIN
Query Match 19.5%; Score 395; DB 8; Length 679;
Best Local Similarity 99.2%; Pred. No. 2.2e-174;
Matches 645; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1161 GTTCTTAAATCAGAGAGACAATTAATCATGTTTCGTGTTTGGAGAGAAGAACA 1220
DB 650 GTTCTTAAATCAGAGAGACAATTAATCATGTTTCGTGTTTGGAGAGAAGAACA 591
QY 1221 GATCAATACGAGAGAGATCTCTAAGAGATTATCGTTTCAAGTAAGTCTCTTATCA 1280
DB 590 GATCAATACGAGAGAGATCTCTAAGAGATTATCGTTTCAAGTAAGTCTCTTATCA 531
QY 1281 AACTCTTAATATAAACAACAAATCAAAACATGAACACGTCGTCTTCGTTTCGATTCTAGAT 1340
DB 530 AACTCTTAATATAAACAACAAATCAAAACATGAACACGTCGTCTTCGTTTCGATTCTAGAT 471
QY 1341 ACCGATTTTGTAGTGTGAATGAACCTCTGTTTATTAATCTACTAGGTTGTTCAATATT 1400
DB 470 ACCGATTTTGTAGTGTGAATGAACCTCTGTTTATTAATCTACTAGGTTGTTCAATATT 411
QY 1401 TTTCGAGAAATTACGAGAGAAACAAGTTAGTGAATATATTTGATGCGAGATGAAGTAA 1460
DB 410 TTTCGAGAAATTACGAGAGAAACAAGTTAGTGAATATATTTGATGCGAGATGAAGTAA 351
QY 1461 TTATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAATATATATAAGAGATT 1520
DB 350 TTATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAATATATATAAGAGATT 291
QY 1521 TTTTGTGTCGAGAAATATGATGAGAAGTTCACTTTTCATATAGTGAACAACCTCTC 1580
DB 290 TTTTGTGTCGAGAAATATGATGAGAAGTTCACTTTTCATATAGTGAACAACCTCTC 231
QY 1581 TTTCATACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCTTTGTCGATTAGGT 1640
DB 230 TTTCATACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCTTTGTCGATTAGGT 171
QY 1641 TAGGTTTGGACTCAGATCAAAATACGATTAGCATACAAATTTTGGCATGCAATTA 1700
DB 170 TAGGTTTGGACTCAGATCAAAATACGATTAGCATACAAATTTTGGCATGCAATTA 111
QY 1701 TTGTCTCAGGTAAATATATACCAATAGAAACATATTTTATAGGAGTAGTTAAGATTATGAT 1760
DB 110 TTGTCTCAGGTAAATATATACCAATAGAAACATATTTTATAGGAGTAGTTAAGATTATGAT 51
QY 1761 TGAAGAAATCTATTACGATAAGCATAAATTTTCTTTGCTGTTCTTGG 1810
DB 50 TGAAGAAATCTATTACGATAAGCATAAATTTTCTTTGCTGTTCTTGG 1

RESULT 3
AQ961293
LOCUS
DEFINITION LERFK31TR LERA Arabidopsis thaliana genomic clone LERFK31, genomic
survey sequence.
ACCESSION AQ961293
VERSION AQ961293.1 GI:6788994
KEYWORDS GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
```

```
REFERENCE 1 (bases 1 to 679)
AUTHORS Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.
TITLE Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
JOURNAL Unpublished (2000)
COMMENT Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For additional information, see http://www.tigr.org/cdb/at/at.html
Seq primer: TR
Class: shotgun.
Location/Qualifiers
1. .679
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERFK31"
/clone_lib="LERA"
/notes="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."

ORIGIN
Query Match 18.1%; Score 368; DB 8; Length 679;
Best Local Similarity 99.3%; Pred. No. 1.1e-161;
Matches 568; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1008 ACCTATTGAGATTGCTTAACCGAACAAGAGGCGTATGACGCCAACGAGGCAAGAGG 1067
DB 70 ACCTATTGAGATTGCTTAACCGAACAAGAGGCGTATGACGCCAACGAGGCAAGAGG 129
QY 1068 GGTAAAAACGAGAAAGAGGCGATGGCAGAAATCGTAATTAACAGGAAAAATAAAGGTGGT 1127
DB 130 GGTAAAAACGAGAAAGAGGCGATGGCAGAAATCGTAATTAACAGGAAAAATAAAGGTGGT 189
QY 1128 TTCACGATAAGTCTGTCTATATGACCGGAAAGAGGTTTCTTAATTCAGAGAGACAATTA 1187
DB 190 CTCACGATAAGTCTGTCTATATGACCGGAAAGAGGTTTCTTAATTCAGAGAGACAATTA 249
QY 1188 TCAGTTTTCGTGTTTGGAGAGAAAGAACAGATCAATACGAGAGAGATCTCTAAA 1247
DB 250 TCAGTTTTCGTGTTTGGAGAGAAAGAACAGATCAATACGAGAGAGATCTCTAAA 309
QY 1248 GAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAACAAACA 1307
DB 310 GAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAACAAACA 369
QY 1308 TGAACACGTCGTCTCTTCGTTTCGATTCAGATACGATTTTTCATGTAATGAAC 1367
DB 370 TGAACACGTCGTCTCTTCGTTTCGATTCAGATACGATTTTTCATGTAATGAAC 429
QY 1368 TCTGTTTATTAATACTAGGTTGTTTCNAATATTTTCCGAGAAATACGAGAGAAACAAG 1427
DB 430 TCTGTTTATTAATACTAGGTTGTTTCNAATATTTTCCGAGAAATACGAGAGAAACAAG 489
QY 1428 TTAGTGATTATATTTGATGACAGAGTGAAGTAATATATATACATAAAATCATGTTTGTCT 1487
DB 490 TTAGTGATTATATTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
QY 1488 CAAGCATCTACGTTGAAATATATATAAGAGAGTTTTCGTTTGGTGAAGAAATATGATGAG 1547
DB 550 CAAGCATCTACGTTGAAATATATATAAGAGAGTTTTCGTTTGGTGAAGAAATATGATGAG 609
QY 1548 AAGTTTCATCTTTTCATTAATAGTGAACAACCTCT 1579
DB 610 AAGTTTCATCTTTTCATTAATAGTGAACAACCTCT 641
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RESULT 4
BZ597205
LOCUS          BZ597205          412 bp      DNA      linear      GSS 07-JAN-2003
DEFINITION    SALK_100410.46.60.n Arabidopsis thaliana T-DNA insertion lines
               Arabidopsis thaliana genomic clone SALK_100410.46.60.n, genomic
               survey sequence.
ACCESSION     BZ597205
VERSION       BZ597205.1  GI:27538158
KEYWORDS      GSS.
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE     1 (bases 1 to 412)
AUTHORS       Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
               Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
               Shinn,P., Zimmerman,J. and Ecker,J.R.
               A Sequence-Indexed Library of Insertion Mutations in the
               Arabidopsis Genome
               Unpublished (2001)
               Contact: Joseph R. Ecker
               Salk Institute Genomic Analysis Laboratory (SIGNAL)
               The Salk Institute for Biological Studies
               10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
               Tel: 858 453 4100 x1752
               Fax: 858 558 6379
               Email: ecker@salk.edu
               This is single pass sequence recovered from the left border of
               TDNA.
               Class: TDNA tagged.
               Location/Qualifiers
                 1. .412
                 /organism="Arabidopsis thaliana"
                 /mol_type="genomic DNA"
                 /ecotype="Col-0"
                 /db_xref="taxon:3702"
                 /clone="SALK_100410.46.60.n"
                 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                 /note="PCR was performed on Arabidopsis thaliana lines
                 each of which contains one or more T-DNA insertion
                 elements. The resultant fragment for each line was
                 directly sequenced to determine the genomic sequence at
                 the site of insertion. Details of the protocols used can
                 be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
  Query Match          12.7%; Score 258; DB 8; Length 412;
  Best Local Similarity 100.0%; Pred. No. 6.8e-110; Indels 0; Gaps 0;
  Matches 258; Conservative 0; Mismatches 0;
  QY 1353 TTCAATGTAAGTGAACCTGTTTATTACTACTAGGTTGTCAATATTTTCCGAGAATT 1412
  Db 32 TTCAATGTAAGTGAACCTGTTTATTACTACTAGGTTGTCAATATTTTCCGAGAATT 91
  QY 1413 ACCAGAGGAACAAAGTTAGTGATTATTGATGCAGAGTATGAAGTAATATATACATAA 1472
  Db 92 ACCAGAGGAACAAAGTTAGTGATTATTGATGCAGAGTATGAAGTAATATATACATAA 151
  QY 1473 ATCATGTTTGTCTCAAGCATCTAGCTGAATATATATAAGAGTTTTCGTTGTTGA 1532
  Db 152 ATCATGTTTGTCTCAAGCATCTAGCTGAATATATATAAGAGTTTTCGTTGTTGA 211
  QY 1533 AAAAAATATGTATGAGAAGTTTCATCTTTTCATAATAGTGAACAACTCTCTTCATACCAA 1592
  Db 212 AAAAAATATGTATGAGAAGTTTCATCTTTTCATAATAGTGAACAACTCTCTTCATACCAA 271
  QY 1593 AAAAAATTTGAAAAAAA 1610
  Db 272 AAAAAAATTTGAAAAAAA 289
RESULT 5
CL489509/c
LOCUS          CL489509          982 bp      DNA      linear      GSS 01-APR-2004
DEFINITION    SAIL_525_C07.v1 SAIL Collection Arabidopsis thaliana genomic clone
               SAIL_525_C07.v1, genomic survey sequence.
ACCESSION     CL489509
VERSION       CL489509.1  GI:45971813
KEYWORDS      GSS.
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE     1 (bases 1 to 982)
AUTHORS       Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
               Dietrich,B., Ho,P., Backaden,J., Ko,C., Clarke,J.D., Cotton,D.,
               Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
               Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
               A high-throughput Arabidopsis reverse genetics system
               Plant Cell 14 (12), 2985-2994 (2002)
               22356987
               MEDLINE
               PUBMED
               COMMENT
               Contact: Sessions A
               Applied Trait Genetics
               Syngenta Biotechnology Inc.
               3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
               Email: allen.sessions@syngenta.com
               ABRC Stock Number CS822250; T-DNA left border flanking sequences of
               Syngenta Arabidopsis Insertion Library (SAIL) lines are available
               through the Arabidopsis Biological Resource Center (ABRC).
               Sequences represent a pool of amplified genomic regions and not
               single contiguous sequences.
               Class: TDNA tagged.
               Location/Qualifiers
                 1. .982
                 /organism="Arabidopsis thaliana"
                 /mol_type="genomic DNA"
                 /ecotype="Columbia"
                 /db_xref="taxon:3702"
                 /clone="SAIL_525_C07.v1"
                 /clone_lib="SAIL Collection"
                 /note="T-DNA left border sequences were isolated using a
                 modified TAIL-PCR strategy"
ORIGIN
  Query Match          5.8%; Score 118; DB 9; Length 982;
  Best Local Similarity 100.0%; Pred. No. 5.2e-44; Indels 0; Gaps 0;
  Matches 118; Conservative 0; Mismatches 0;
  QY 1218 ACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAGTCTCTTTA 1277
  Db 175 ACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAGTCTCTTTA 116
  QY 1278 TCAAACTCTTATATAAACAATCAAAACATGAACACGTCGTCTGTTCTGTTTCGATTTC 1335
  Db 115 TCAAACTCTTATATAAACAATCAAAACATGAACACGTCGTCTGTTCTGTTTCGATTTC 58
RESULT 6
CR402809
LOCUS          CR402809          194 bp      DNA      linear      GSS 02-MAY-2004
DEFINITION    Arabidopsis thaliana T-DNA flanking sequence GK-858C06-025968,
               genomic survey sequence.
ACCESSION     CR402809
VERSION       CR402809.1  GI:46943537
KEYWORDS      GSS.
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE     1
AUTHORS       Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
               GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
```

the identification of T-DNA insertion mutants in Arabidopsis thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 22755829
 12874060
 2
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 23117147
 14756321
 3
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 14682050
 4 (bases 1 to 194)
 Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
 Direct Submission
 Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At4g20250.
 Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers
 1..194
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-858C06-025968"
 /ecotype="Col-0"
 /notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 5.5%; Score 112; DB 9; Length 194;
 Best Local Similarity 100.0%; Pred. No. 3.7e-41;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 784 ATATTGCCAAGTGTGATGTCAGTGCAGTGCAGTGCATATTTCCCTCCCTGATTACG 843
 Db 83 ATATTGCCAAGTGTGATGTCAGTGCAGTGCAGTGCATATTTCCCTCCCTGATTACG 142
 Qy 844 TTTTACCCCTTCCTCTCTCTGTTTCCACCGTTAATTCAATTTACTATTGTA 895
 Db 143 TTTTACCCCTTCCTCTCTCTGTTTCCACCGTTAATTCAATTTACTATTGTA 194

RESULT 7
 BH809771 246 bp DNA linear GSS 02-MAY-2002
 LOCUS
 DEFINITION
 SALK_005656 Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK_005656, genomic survey sequence.
 BH809771
 ACCSSION
 BH809771.1 GI:20387588
 VERSION
 KEYWORDS
 SOURCE
 Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 246)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

REFERENCE

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

This is single pass sequence recovered from the left border of T-DNA. This sequence lies within an annotated exon of At4g20250.

FEATURES

Location/Qualifiers
 1..246
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_005656"
 /notes="PCR was performed on Arabidopsis thaliana T-DNA insertion lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 5.1%; Score 103; DB 8; Length 246;
 Best Local Similarity 100.0%; Pred. No. 6.2e-37;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 903 CTTTCACCTTTTAAAGAAACCCACCGAAATCATATACCGAAATCATGTCT 962
 Db 49 CTTTCACCTTTTAAAGAAACCCACCGAAATCATATACCGAAATCATGTCT 108
 Qy 963 TCATGTGACGTACAGACTATTTTCGGTTGAATTTGGTT 1005
 Db 109 TCATGTGACGTACAGACTATTTTCGGTTGAATTTGGTT 151

RESULT 8

CC796100/c
 LOCUS
 DEFINITION
 SALK_092760.46.60.n Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK_092760.46.60.n, genomic survey sequence.

ACCESSION

CC796100

VERSION

CC796100.1 GI:32391323

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 396)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g20250.

Class: TDNA tagged.
Location/Qualifiers
1. .396
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_092760.46.60.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES

source

ORIGIN

Query Match 4.7%; Score 95; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.6e-33; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 0;
QY 381 TTTTCCATCTCGATGGTTTTCGTTCCGTTGAACCAATTCACACITTTGTATTAACCG 440
Db 162 TTTTCCATCTCGATGGTTTTCGTTCCGTTGAACCAATTCACACITTTGTATTAACCG 103
QY 441 AATAGTATATCTAGACGTAGCCCAATACCAAAA 475
Db 102 AATAGTATATCTAGACGTAGCCCAATACCAAAA 68

RESULT 9

AV832342
LOCUS AV832342 RAFL11 Arabidopsis thaliana cDNA clone RAFL11-12-C05 5',
DEFINITION mRNA sequence.

ACCESSION AV832342 GI:19874402

VERSION AV832342

SOURCE EST.

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished (2002)

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msekirc@riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda E1C-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pluscript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES

source

Location/Qualifiers

1. .207

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="RAFL11-12-C05"

/dev_stage="plants at various developmental stages from

germination to mature seeds"

/lab_host="DH10B"

/clone_lib="RAFL11"

/note="Site 1: BamHI; Site 2: SalI; subjected to various

treatments (dehydration, cold, high salt, ABA, heat and

UV). Dark-grown plants"

ORIGIN

Query Match 4.3%; Score 88; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.2e-30; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 0;
QY 1177 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 1236
Db 2 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 61
QY 1237 AGATCTCTAAAGAGATTATCGTTTCAA 1264
Db 62 AGATCTCTAAAGAGATTATCGTTTCAA 89

RESULT 10

AJ609323

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AJ609323 278 bp mRNA linear EST 09-JAN-2004
AJ609323 Arabidopsis thaliana aerial vegetative tissues 4-weeks old
Arabidopsis thaliana cDNA clone al89D6 5', mRNA sequence.

AJ609323

EST.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 278)

Clepet,C., Le Clainche,I. and Caboche,M.

Improved full-length cDNA production based on RNA tagging by T4 DNA

ligase

Nucleic Acids Res. 32 (1), E6 (2004)

Contact: Clepet CY

URGV, CNRS / INRA

2 Rue Gaston-Cremlieux, 91057 Evry, France.

Location/Qualifiers

1. .278

source

FEATURES

source

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="al89D6"

/tissue_type="aerial vegetative tissues"

/dev_stage="4-weeks old"

/clone_lib="Arabidopsis thaliana aerial vegetative tissues

4-weeks old"

/note="ecotype: Columbia 0 ; country: France"

ORIGIN

Query Match 4.3%; Score 86; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 7.1e-30; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 0;
QY 1177 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 1236
Db 1 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 60
QY 1237 AGATCTCTAAAGAGATTATCGTTTCAA 1264
Db 61 AGATCTCTAAAGAGATTATCGTTTCAA 88


```

RESULT 11
AV825689      507 bp  mRNA  linear  EST 01-APR-2002
LOCUS        AV825689 RAFL7 Arabidopsis thaliana cDNA clone RAFL07-12-M18 5',
DEFINITION   mRNA sequence.
ACCESSION    AV825689
VERSION      AV825689.1 GI:19867749
KEYWORDS     EST
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE    1 (bases 1 to 507)
AUTHORS      Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
              Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
              Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
              and Shinozaki,K.
              Large scale analysis of Arabidopsis full-length cDNA (2002b)
              Unpublished (2002)
              Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: msek@rc.riken.go.jp
              An Arabidopsis full-length cDNA library was constructed essentially
              as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
              and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
              al., submitted for publication) digested with BamHI and SalI. This
              clone is in a modified pluscript vector. Please visit our web
              site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
              details.
FEATURES     source
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                cold-treated (1, 2, 5, 10, 24 hr)"
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Best Local Similarity 100.0%; Pred. No. 7e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1177 GAGCAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 1236
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Db 63 AGATCTCTAAGAGATTATCGTTTCAA 90
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BP562932/c    605 bp  mRNA  linear  EST 20-JUN-2004
LOCUS        BP562932 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-39-009 5',
DEFINITION   mRNA sequence.
ACCESSION    BP562932
VERSION      BP562932.1 GI:48978698
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SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
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              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

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REFERENCE    1 (bases 1 to 605)
AUTHORS      Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
              Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
              Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
              Arakawa,T., Shibata,K., Shinagawa,A., and Shinozaki,K.
              Functional annotation of a full-length Arabidopsis cDNA collection
              Science 296 (5565), 141-145 (2002)
              MEDLINE 21932900
              PUBMED 11910074
              Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: msek@rc.riken.go.jp
              Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
              further details.
FEATURES     source
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ORIGIN
Query Match 4.2%; Score 86; DB 5; Length 605;
Best Local Similarity 100.0%; Pred. No. 6e-29;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1179 GACAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 1238
Db 395 GACAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 336
QY 1239 ATCTCTAAGAGATTATCGTTTCAA 1264
Db 335 ATCTCTAAGAGATTATCGTTTCAA 310
RESULT 13
T43139
LOCUS        T43139 463 bp  mRNA  linear  EST 06-NOV-1997
DEFINITION   6402 Lambda-PRL2 Arabidopsis thaliana cDNA clone 115M24T7, mRNA
              sequence.
              T43139
              VERSION T43139.1 GI:25977703
              EST.
              SOURCE Arabidopsis thaliana (thale cress)
              ORGANISM Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
              1 (bases 1 to 463)
              Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
              McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
              Retzel,E. and Somerville,C.
              Genes galore: a summary of methods for accessing results from
              large-scale partial sequencing of anonymous Arabidopsis cDNA clones
              Plant Physiol. 106, 1241-1255 (1994)
              MEDLINE 95148729
              PUBMED 7846151
              On Nov 6, 1997 this sequence version replaced gi:933425.
              Contact: Thomas Newman
              MSU-DOE Plant Research Laboratory
              Michigan State University
              MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
              Lansing, MI
              Tel: 517-353-0854
              Fax: 517-353-9168
              Email: 22313tcn@ibm.cl.msu.edu

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FEATURES
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        Lambda PRL2 is a cDNA library derived from equal
        quantities of 4 pools of mRNA. The mRNA sources were 1) 7
        day germinated etiolated seedlings; 2) tissue culture
        grown roots; 3) staged plants half with 24 hour light
        cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
        same plants as 3 but aerial tissue (stems, flowers and
        siliques). The vector is BRL's lambda Zip-Lox. The cDNA
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QY 1181 CAATTAATCAGTTTCGTGTGTTGGAGAGAAGAACAGATCAAAATACGAGGAGAT 1240
Db      1 CAATTAATCAGTTTCGTGTGTTGGAGAGAAGAACAGATCAAAATACGAGGAGAT 60

QY 1241 CTCTAAGAGATTTATCGTTTCAA 1264
Db      61 CTCTAAGAGATTTATCGTTTCAA 84

RESULT 14
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DEFINITION 6413 Lambda-PRL2 Arabidopsis thaliana cDNA clone 115N24T7, mRNA
ACCESSION T43150
VERSION T43150.1 GI:933436
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 495)
AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
PUBMED 7846151
COMMENT
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7 dye primer.
On Apr 14, 1993 this sequence version replaced gi:635738.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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        quantities of 4 pools of mRNA. The mRNA sources were 1) 7
        day germinated etiolated seedlings; 2) tissue culture
        grown roots; 3) staged plants half with 24 hour light
        cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
        same plants as 3 but aerial tissue (stems, flowers and
        siliques). The vector is BRL's lambda Zip-Lox. The cDNA
        inserts were directionally cloned with Sal-Not arms using
        oligo dT primed cDNA. "
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QY 1181 CAATTAATCAGTTTCGTGTGTTGGAGAGAAGAACAGATCAAAATACGAGGAGAT 1240
Db      1 CAATTAATCAGTTTCGTGTGTTGGAGAGAAGAACAGATCAAAATACGAGGAGAT 60

QY 1241 CTCTAAGAGATTTATCGTTTCAA 1264
Db      61 CTCTAAGAGATTTATCGTTTCAA 84

RESULT 15
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DEFINITION 14873 Lambda-PRL2 Arabidopsis thaliana cDNA clone 178C4T7, mRNA
ACCESSION H36351
VERSION H36351.1 GI:905850
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 516)
AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
PUBMED 7846151
COMMENT
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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    Lambda PRL2 is a cDNA library derived from equal
    quantities of 4 pools of mRNA. The mRNA sources were 1) 7
    day germinated etiolated seedlings; 2) tissue culture
    grown roots; 3) staged plants half with 24 hour light
    cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
    same plants as 3 but aerial tissue (stems, flowers and
    siliques). The vector is BRL's lambda Zip-Lox. The cDNA
    inserts were directionally cloned with Sal-Not arms using
    oligo dT primed cDNA. "

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inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA. "

ORIGIN

Query Match 4.1%; Score 83; DB 7; Length 516;
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DB 61 TCTAAAGAGATTTATCGTTTCAA 83

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